

GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 28, 2004, 07:08:10 ; Search time 590 Seconds  
(without alignments)

9437.043 Million cell updates/sec

Title: US-10-620-845-8

Perfect score: 1224

Sequence:

1 atgggagcacaacttcaag.....agatctcgaaagtctcataa 1224

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Sequences: 2960401 seqs, 2274450654 residues

Total number of hits satisfying chosen parameters: 5920802

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Lasting first 45 summaries

Database:

Published Applications NA.\*  
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19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1224	100.0	1224	9	US-09-841-683-8
2	1224	100.0	1675	9	Sequence 8, Appli
3	1165.4	95.2	1191	9	Sequence 12, Appl
4	1165.4	95.2	1594	13	Sequence 10, Appl
5	1165.4	95.2	1594	13	Sequence 44, Appl
6	1165.4	95.2	1594	13	Sequence 1, Appli
7	1163.8	95.1	1281	16	Sequence 44, Appl
8	1163.8	95.1	1281	16	Sequence 102, Appl
9	1160.6	94.8	1485	9	Sequence 100, App
10	1160.6	94.8	1485	13	Sequence 1, Appli
11	1160.6	94.8	1485	13	Sequence 1, Appli
12	1032.2	84.3	2083	16	Sequence 231, App
13	672.8	55.0	678	13	Sequence 239, App
14	661	54.0	711	9	Sequence 6, Appli

15	650	53.9	678	9	US-09-841-683-4	Sequence 4, Appli
16	542.4	44.3	3224	13	US-10-342-887-1782	Sequence 1782, Ap
17	542.4	44.3	3224	13	US-10-172-118-1782	Sequence 1782, Ap
18	542.4	44.3	3224	15	US-10-161-803-40	Sequence 40, Appl
19	542.4	44.3	3224	15	US-10-354-358-35	Sequence 35, Appl
20	519.6	42.5	3244	13	US-10-206-915-571	Sequence 571, App
21	519.6	42.5	3244	13	US-10-199-670-571	Sequence 571, App
22	519.6	42.5	3244	13	US-10-201-858-571	Sequence 571, App
23	519.6	42.5	3244	13	US-10-205-830-571	Sequence 571, App
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25	519.6	42.5	3244	13	US-10-201-853-571	Sequence 571, App
26	519.6	42.5	3244	13	US-10-174-581-571	Sequence 571, App
27	519.6	42.5	3244	13	US-10-176-483-571	Sequence 571, App
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35	519.6	42.5	3244	13	US-10-187-740-571	Sequence 571, App
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42	519.6	42.5	3244	13	US-10-195-896-571	Sequence 571, App
43	519.6	42.5	3244	13	US-10-196-744-571	Sequence 571, App
44	519.6	42.5	3244	13	US-10-196-755-571	Sequence 571, App
45	519.6	42.5	3244	13	US-10-196-757-571	Sequence 571, App

#### ALIGNMENTS

#### RESULT 1

US-09-841-683-8

; Sequence 8, Application US/09841683

; Patent No. US20030081600A1

; GENERAL INFORMATION:

; APPLICANT: Hu, Yi

; APPLICANT: Nepomichy, Boris

; APPLICANT: Wang, Xiaoming

; APPLICANT: Donoho, Gregory

; APPLICANT: Scoville, John

; APPLICANT: Walke, D. Wade

; TITLE OF INVENTION: No. US20020081600A1el Human Kinase Proteins and Polynucleotides Er

; FILE REFERENCE: LEX-0167-USA

; CURRENT APPLICATION NUMBER: US/09/841,683

; CURRENT FILING DATE: 2001-04-24

; PRIOR APPLICATION NUMBER: US 60/199,499

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: US 60/201,227

; PRIOR FILING DATE: 2000-05-01

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 8

; LENGTH: 1224

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-841-683-8

Query Match 100.0%; Score 1224; DB 9; Length 1224;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGAGCACAACCTTCAAGAAAACCCAGCTGTTTGATGAAAAATGAAGATGTCACACTTT 60

1 ATGGGAGCACAACCTTCAAGAAAACCCAGCTGTTTGATGAAAAATGAAGATGTCACACTTT 60

QY 61 GACCACTTGAATTTTGGAGCCATTTGGGAAGGCAGTTTGGGAGCTTCGATGTA 120

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61 GACCACTTTGAAATTTTCGGAGCCATTCGGAAAGCCAGTCTTTGGGAGGCTCTGCATGTA 120

121 CAGAGAAGATGATACCAAGAAGATGATGCAATGAAGTACATGAATAAACAAGAGTGGGTG 180

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181 GAGCGCATGAAATGAGAAATGCTCTTCAAGGAACCTCCAGATCATGCGGGTCTCGAGCAC 240

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301 GACCTCTCTGGTGGAGACCTGGTATTCCTTCCAGATGAGGAAGACATGTTTCATGGTGGTG 360

361 GAAAAGTGAAGCTCTTTCATCTGTGAGCTGGTCTGAGTCCCTGGATCTTACCTGCAGAACCCAG 420

361 GAAAAGTGAAGCTCTTTCATCTGTGAGCTGGTCTGAGTCCCTGGATCTTACCTGCAGAACCCAG 420

421 CGCATCATTCACAGGATATGAAGCTGTCAATATTTTACTTTGAAGAAATGAGGAAGACATGTTTCATGGTGGTG 480

421 CGCATCATTCACAGGATATGAAGCTGTCAATATTTTACTTTGAAGAAATGAGGAAGACATGTTTCATGGTGGTG 480

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781 CTGCAACTAACTCAGACCAAGATTTCTCAGTATCTGATCTCAGAACTTCCGAT 840

781 CTGCAACTAACTCAGACCAAGATTTCTCAGTATCTGATCTCAGAACTTCCGAT 840

841 ATGAATGATATAACTGGGATGAGTTCAGAGAGGCTCATTTCCAGTTCATTCCT 900

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901 AATAAGGCGAGCTGAATCTGATCTTACCTTTGAATCTGAGAAATGATTTTGGAGTCC 960

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Db 12C1 TTTCAGACCTCGAAAGTTTCATAA 1224

## RESULT 2

```

RESULT 2
US-09-841-683-12
; Sequence 12, Application US/09841683
; Patent No. US20020081600A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnuchy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. US20020081600A1el Human Kinase Proteins and Polynucleotides Er
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1675
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-841-683-12

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Query Match	100.0%;	Score 1224;	DB 9;	Length 1675;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1224;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps	0;			

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DB	473	GACCAC	TTTGAAA	TTTTGCGAG	CCATTGGG	AAAGCG	AGTTTGGG	AAAGTCTGCA	532
QY	121	CAGAAG	ATGAT	ACAGAA	GATGTAC	CCCAAT	GAAGTAC	ATGAATAA	180
DB	533	CAGAAG	ATGAT	ACAGAA	GATGTAC	CCCAAT	GAAGTAC	ATGAATAA	592
QY	181	GAGCG	CAATGA	AGTGAG	AAATGTCTT	CAAGGAA	CTCCAG	ATCATCAG	240
DB	593	GAGCG	CAATGA	AGTGAG	AAATGTCTT	CAAGGAA	CTCCAG	ATCATCAG	652
QY	241	CC	TTTCC	TGGTTAA	TTTGTG	GTATTC	TTCC	MA	300
DB	653	CC	TTTCC	TGGTTAA	TTTGTG	GTATTC	TTCC	MA	712
QY	301	GACCT	CCCTG	CTGGG	TGGAG	ACTGG	GTATCAC	CTGCAACAG	360
DB	713	GACCT	CCCTG	CTGGG	TGGAG	ACTGG	GTATCAC	CTGCAACAG	772
QY	361	GA	AA	CAGTGA	AGCTCTT	CATCTG	TGAG	CTGTC	420
DB	773	GA	AA	CAGTGA	AGCTCTT	CATCTG	TGAG	CTGTC	832
QY	421	CG	CAT	CA	TTCCAG	GGATATGA	AGCGT	CACATAT	480
DB	833	CG	CAT	CA	TTCCAG	GGATATGA	AGCGT	CACATAT	892
QY	481	CA	CAT	CACAG	ATTTCA	ACAT	TGCTG	CGATG	540
DB	893	CACAT	CACAG	ATTTCA	ACAT	TGCTG	CGATG	CGCCAGG	952







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Db

RESULT 5  
US-10-182-243-1  
Sequence 1, Application US/10182243  
Publication No. US20040048310A1  
GENERAL INFORMATION:  
APPLICANT: PLOWMAN, GREGORY D.  
APPLICANT: WHYTE, DAVID  
APPLICANT: MANNING, GERARD  
APPLICANT: SUDARSANAM, SUCHA  
APPLICANT: MARTINEZ, RICARDO  
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE  
TITLE OF INVENTION: ENZYMES  
FILE REFERENCE: 038602/1366  
CURRENT APPLICATION NUMBER: US/10/182,243  
CURRENT FILING DATE: 2003-07-07  
PRIOR APPLICATION NUMBER: PCT/US01/02337  
PRIOR FILING DATE: 2001-01-25  
NUMBER OF SEQ ID NOS: 84  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 1  
LENGTH: 1594  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-182-243-1

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464 GACCACTTGAATTTTGGAGCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 523  
121 CAGAAAGATGATACCAAGAGAGTGTACGCAATGACATGATGATGATGATGATGATGATGATG 180  
524 CAGAAAGATGATACCAAGAGAGTGTACGCAATGACATGATGATGATGATGATGATGATGATG 583  
181 GAGCGCAATGAGTGAAGAAATGCTTCAAGGAACTCCAGATCATGACAGGCTCTGGAGCAC 240  
584 GAGCGCAATGAGTGAAGAAATGCTTCAAGGAACTCCAGATCATGACAGGCTCTGGAGCAC 643  
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644 CCTTCTCTGTTAAATTTGTTGTTATCTTCCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 703  
301 GACCTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 360  
704 GACCTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 763  
361 GAAACAGTGAAGCTTTCATCTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 420  
764 GAAACAGTGAAGCTTTCATCTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 823  
421 CGCATCATTCACAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480  
824 CGCATCATTCACAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 883  
481 CACATCAGATTTCAACATGCTGCGATGCTGCGATGCTGCGATGCTGCGATGCTGCGATGCTG 540  
884 CACATCAGATTTCAACATGCTGCGATGCTGCGATGCTGCGATGCTGCGATGCTGCGATGCTG 943  
541 GCTGGCACCAGCCTTACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 600

944 GCTGGCACCAGGCTTACATGCGCACCTGAGATGTTGAGTCCAGAACAGAGGAGGAGGAT 1003  
601 TCCTTTGCTGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
1004 TCCTTTGCTGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1063  
661 AGACCGTATCATATTCGCTCCAGTACTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720  
1064 AGACCGTATCATATTCGCTCCAGTACTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1123  
721 ACTGTTGTAACCTTACCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
1124 ACTGTTGTAACCTTACCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1183  
781 CTCGAACCTATTCAGACCAACGATTTTCTCAGTATCTGATGCTGATGCTGATGCTGATGCTGATG 840  
1184 CTCGAACCTATTCAGACCAACGATTTTCTCAGTATCTGATGCTGATGCTGATGCTGATGCTGATG 1243  
841 ATGAATGATATAAATCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
1244 ATGAATGATATAAATCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1303  
901 AATAAGGCGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
1304 AATAAGGCGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1363  
961 AAACCTCTACATAAGAAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020  
1364 AAACCTCTACATAAGAAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1423  
1021 GATTTCTCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
1424 GATTTCTCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1483  
1081 ATTTTCAACAGAGAAAAGTAAACAGGAGCTTAAACAGGAGCTTAAACAGGAGCTTAAACAGGAG 1140  
1484 ATTTTCAACAGAGAAAAGTAAACAGGAGCTTAAACAGGAGCTTAAACAGGAGCTTAAACAGGAG 1543  
1141 GAACAAACCAAGAGCCACCAAGTGCACAAATGGACAATGGACA 1183  
1544 GAACAAACCAAGAGCCACCAAGTGCACAAATGGACAATGGACA 1586

Db

RESULT 6  
US-10-288-793-44  
Sequence 44, Application US/10288798  
Publication No. US20030207299A1  
GENERAL INFORMATION:  
APPLICANT: BANDMAN, Olga; NGUYEN, Dannie B;  
APPLICANT: WALIA, Narinder K.; HAFALIA, April J.A.;  
APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;  
APPLICANT: GURURAJAN, Rajagopal; DING, Li;  
APPLICANT: PATTERSON, Chandra; YUE, Henry;  
APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;  
APPLICANT: THORNTON, Michael; ELLIOTT, Vicki S.;  
APPLICANT: LU, Yan; ISON, Craig H.;  
APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;  
APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;  
APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;  
APPLICANT: LU, Dvyn Aina M.; LAL, Preeti G.;  
APPLICANT: RAMKUMAR, Jayalaxmi; WARREN, Bridget A.;  
APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;  
APPLICANT: THANGAVELU, Kavitha; BURFORD, Neil  
TITLE OF INVENTION: HUMAN KINASES  
FILE REFERENCE: PI-0209 USA  
CURRENT APPLICATION NUMBER: US/10/288,798  
CURRENT FILING DATE: 2002-11-01  
PRIOR APPLICATION NUMBER: PCT/US01/27219  
PRIOR FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: US 60/240,542  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: US 60/238,389  
PRIOR FILING DATE: 2000-10-06

Copied from 10260845 on 08/11/2005

; PRIOR FILING DATE: 2001-02-16  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 136  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 102  
 ; LENGTH: 1191  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)...(1191)  
 ; us-10-410-764-102

Query Match 95.1%; Score 1163.8; DB 16; Length 1191;  
 Best Local Similarity 99.0%; Pred. No. 0;  
 Matches 1171; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
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 1 ATGGGAGCCAACTTCAAGAAACCAACAGAGTGTGGTGAATGAAGATGTCACATTT 60  
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 61 GACCACTTTGAATTTTGGAGCCATTGGGAAGGAGTGTGGGAGGCTGTCATTTGA 120  
 121 CAGAAGATGATACCAAGAGATGTACGCAATGAAGTACATGAATTAACAAAGTGGTG 180  
 121 CAGAAGATGATACCAAGAGATGTACGCAATGAAGTACATGAATTAACAAAGTGGTG 180  
 181 GAGCGCAATGAAGTGAAGAAATGCTTCAAGAACTCCAGATCATGAGGGTCTGGAGCAC 240  
 181 GAGCGCAATGAAGTGAAGAAATGCTTCAAGAACTCCAGATCATGAGGGTCTGGAGCAC 240  
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 421 CGCATCATTCACAGGATATGAAGCTTGAATTTTACTTACCAAGACATGCGGACCTG 480  
 481 CACATCACAGATTTCAACATTTGCGGATGCTGCCAGGAGACACAGATTTACCACATG 540  
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 541 GCTGGGACCAAGCTTACATGCGACCTGAGATGTTGCTCCAGAAAGGAGGAGGCTAT 600  
 541 GCTGGGACCAAGCTTACATGCGACCTGAGATGTTGCTCCAGAAAGGAGGAGGCTAT 600  
 601 TCCTTTGCTGTTGACTGTTGCTGCTGCGGAGTGAAGGATGATGATGCTGAGAGGCGG 660  
 601 TCCTTTGCTGTTGACTGTTGCTGCTGCGGAGTGAAGGATGATGATGCTGAGAGGCGG 660  
 661 AGACCGGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACAGTTTGAGCG 720  
 661 AGACCGGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACAGTTTGAGCG 720  
 721 ACTGTTGTAATCTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
 721 ACTGTTGTAATCTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
 781 CTGGAACCTAATCCAGACCAAGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT 840  
 781 CTGGAACCTAATCCAGACCAAGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT 840

841 ATGAATGATATAAATCTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
 841 ATGAATGATATAAATCTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
 901 AATAAGGAGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
 901 AATAAGGAGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
 961 AAACCTCTACATAAGAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
 961 AAACCTCTACATAAGAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
 1021 GATTTCTCTCAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
 1021 GATTTCTCTCAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
 1081 ATTTTCAACAGAGAAAGTAAACAGGAGTAAACAGGAGTAAACAGGAGTAAACAGGAGTAA 1140  
 1081 ATTTTCAACAGAGAAAGTAAACAGGAGTAAACAGGAGTAAACAGGAGTAAACAGGAGTAA 1140  
 1141 GAACAAACCAAGAGCCCAAGTGAACAAATGGAACAAATGGAACAAATGGAACAAATGGAAC 1183  
 1141 GAACAAACCAAGAGCCCAAGTGAACAAATGGAACAAATGGAACAAATGGAACAAATGGAAC 1183

RESULT 8  
 US-10-410-764-100  
 ; Sequence 100, Application US/10410764  
 ; Publication No. US20040005664A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Millennium Pharmaceuticals, Inc.  
 ; APPLICANT: Meyers, Rachel E.  
 ; APPLICANT: MacBeth, Kyle J.  
 ; APPLICANT: Curtis, Rory A.J.  
 ; APPLICANT: Rudolph-Owen, Laura A.  
 ; APPLICANT: Weich, Nadine S.  
 ; APPLICANT: Olandt, Peter J.  
 ; APPLICANT: Tsai, Fong-Ying  
 ; APPLICANT: Kapeller-Libermann, Rosana  
 ; APPLICANT: Carroll, Joseph M.  
 ; TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226.  
 ; TITLE OF INVENTION: 58764, 62113, 32144, 32235, 23565, 13305, 14911, 86216,  
 ; FILE REFERENCE: 25206 AND 8843 MOLECULES AND USES THEREFOR  
 ; CURRENT APPLICATION NUMBER: US/10/410,764  
 ; PRIOR FILING DATE: 2003-04-10  
 ; PRIOR APPLICATION NUMBER: US 09/924,358  
 ; PRIOR FILING DATE: 2001-08-06  
 ; PRIOR APPLICATION NUMBER: US 60/229,300  
 ; PRIOR FILING DATE: 2000-09-01  
 ; PRIOR APPLICATION NUMBER: US 10/350,553  
 ; PRIOR FILING DATE: 2003-01-24  
 ; PRIOR APPLICATION NUMBER: US 60/351,572  
 ; PRIOR FILING DATE: 2002-01-24  
 ; PRIOR APPLICATION NUMBER: US 09/966,614  
 ; PRIOR FILING DATE: 2001-09-27  
 ; PRIOR APPLICATION NUMBER: US 60/238,054  
 ; PRIOR FILING DATE: 2000-10-05  
 ; PRIOR APPLICATION NUMBER: US 10/281,094  
 ; PRIOR FILING DATE: 2002-10-25  
 ; PRIOR APPLICATION NUMBER: US 60/347,815  
 ; PRIOR FILING DATE: 2001-10-29  
 ; PRIOR APPLICATION NUMBER: US 10/076,535  
 ; PRIOR FILING DATE: 2002-02-15  
 ; PRIOR APPLICATION NUMBER: US 60/269,440  
 ; PRIOR FILING DATE: 2001-02-16  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 136  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 100  
 ; LENGTH: 1281  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (49)...(1239)
US-10-410-764-100

Query Match
Best Local Similarity 95.18; Score 1163.8; DB 16; Length 1281;
Matches 1171; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ATGGAGCCCAACACTTCAAGAAACCCACAGTGTGTTGATGAATAAGATGTCACATTT 60
DB 49 ATGGAGCCCAACACTTCAAGAAACCCACAGTGTGTTGATGAATAAGATGTCACATTT 108
QY 61 GACCACTTGAATTTGCGAGCCATTTGGAAAGGCGAGTTTGGGAAGGTCGATTTGTA 120
DB 109 GACCACTTGAATTTGCGAGCCATTTGGAAAGGCGAGTTTGGGAAGGTCGATTTGTA 168
QY 121 CAGAAGATGATCAACAGAGATGTAGCAATGAAGTACATGAATAACAAAGTGGTG 180
DB 169 CAGAAGATGATCAACAGAGATGTAGCAATGAAGTACATGAATAACAAAGTGGTG 228
QY 181 GAGCGCAATGAAGTGAAGAAATGTCTTCAAGGAACCTCCAGATCATGCGGGTCTGGAGCAC 240
DB 229 GAGCGCAATGAAGTGAAGAAATGTCTTCAAGGAACCTCCAGATCATGCGGGTCTGGAGCAC 288
QY 241 CTTTCTCTGTTAATTTGTGTTATCTTCCAGATGAGGAAGACATGTTTCATGTTGGTG 300
DB 289 CTTTCTCTGTTAATTTGTGTTATCTTCCAGATGAGGAAGACATGTTTCATGTTGGTG 348
QY 301 GACCTCTGCTGGTGGAGACCTCGTTTATCACCTGCAACAGAGACCTCCACTTCAAGAA 360
DB 349 GACCTCTGCTGGTGGAGACCTCGTTTATCACCTGCAACAGAGACCTCCACTTCAAGAA 408
QY 361 GAAACAGTGAAGCTCTTCACTGTGAGCTGTGATGCGCCCTGGACTACCTGCAAGAACAG 420
DB 409 GAAACAGTGAAGCTCTTCACTGTGAGCTGTGATGCGCCCTGGACTACCTGCAAGAACAG 468
QY 421 CGCATATATCAAGGATATGAAGCTGACAAATATTTTACTGTAGCAACATGCGGACATG 480
DB 469 CGCATATATCAAGGATATGAAGCTGACAAATATTTTACTGTAGCAACATGCGGACATG 528
QY 481 CACATCAAGATTTCAACATTTGCGGATGCTGCGGAGGAGACACAGATTTACCAACATG 540
DB 529 CACATCAAGATTTCAACATTTGCGGATGCTGCGGAGGAGATGACAGATTTACCAACATG 588
QY 541 GCTGGCAACCAAGCCTTACATGCGACCTGAGATGTTTCACTCCAGAAAGGAGGAGCTAT 600
DB 589 GCTGGCAACCAAGCCTTACATGCGACCTGAGATGTTTCACTCCAGAAAGGAGGAGCTAT 648
QY 601 TCCTTTGCTGTGACTGTGTTGCTGCGGAGTACGCGCATATGACTGCTGAGAGGCGG 660
DB 649 TCCTTTGCTGTGACTGTGTTGCTGCGGAGTACGCGCATATGACTGCTGAGAGGCGG 708
QY 661 AGACGATATCATTTTCCAGTACTTCCAGCAAGGAAATTTTACACACCTTTGAGACG 720
DB 709 AGACGATATCATTTTCCAGTACTTCCAGCAAGGAAATTTTACACACCTTTGAGACG 768
QY 721 ACTGTGTAACTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 769 ACTGTGTAACTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 828
QY 781 CTCGAACCTATATCAAGCAAGATTTTCTGATTTATCTGATGTCAGAACTTCCCGTAT 840
DB 829 CTCGAACCTATATCAAGCAAGATTTTCTGATTTATCTGATGTCAGAACTTCCCGTAT 888
QY 841 ATGAATGATATAAATCGGATCGAGTTTTCAGAAAGGCTCATTTCCAGGTTTCAATTCCT 900
DB 889 ATGAATGATATAAATCGGATCGAGTTTTCAGAAAGGCTCATTTCCAGGTTTCAATTCCT 948
QY 901 AATAAGGAGGCTGAAATTTGATCCTTACCTTTGAACTTTGAGAAATGATTTGGAGTCC 960
DB 949 AATAAGGAGGCTGAAATTTGATCCTTACCTTTGAACTTTGAGAAATGATTTGGAGTCC 1008

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Db 1093 ATTTTCAAGAGAAAAGTAAACAGGAGCTTTTAAACAAAGACAAACCAAAATCTAGCCTTG 1142  
Qy 1141 GAACAAACCAAGACCCCAAGTGAACAAATGACAAATGGGACA 1183  
Db 1143 GAACAAACCAAGACCCCAAGTGAACAAATGAGATGGTCAAGATAACA 1185

RESULT 11  
US-10-254-869-1  
; Sequence 1, Application US/10254869  
; Publication No. US20030027307A1  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001160DIV  
; CURRENT APPLICATION NUMBER: US/10/254,869  
; CURRENT FILING DATE: 2002-09-26  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1485  
; TYPE: DNA  
; ORGANISM: Human  
us-10-254-869-1

Query Match 94.8%; Score 1160.6; DB 15; Length 1485;  
Best Local Similarity 98.8%; Pred. No. 0;  
Matches 1169; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

1 ATGGGAGCCAACTTCAAGAAAACCCAGGTGTTGATGAATAATGAAGATGTCAACTTT 60  
3 ATGGGAGCGAACACTTCAAGAAAACCCAGGTGTTGATGAATAATGAAGATGTCAACTTT 62  
61 GACCACTTTGAAATTTTGGGAGCCATGGGAAGCAGTTTTGGGAAGGTCTGCATTGTA 120  
63 GACCACTTTGAAATTTTGGGAGCCATGGGAAGCAGTTTTGGGAGGTCTGCATTGTA 122  
121 CAGAAAGATGATACCAAGAGATGTACGCAATGAAGTACATGAATAAACAAGAGTGGTG 180  
123 CAGAAAGATGATACCAAGAGATGTGGCAATGAAGTACATGAATAAACAAGAGTGGTG 182  
181 GAGCCAAATGAAGTGAAGAAATGTCTTCAAGGAATCTCCAGATCATCGAGGTCTGGAGCAC 240  
183 GAGCCAAATGAAGTGAAGAAATGTCTTCAAGGAATCTCCAGATCATCGAGGTCTGGAGCAC 242  
241 CCTTTCTCTGTTAAATTTGTTGTTTCTTCCAGATGAGGAGACATGTTCAATGTTGGTG 300  
243 CCTTTCTCTGTTAAATTTGTTGTTTCTTCCAGATGAGGAGACATGTTCAATGTTGGTG 302  
301 GACCTCTCTGCTGGGTGGAGACCTGGGTTATCACTTCCAGCAAGACGTCCACTTCAAGGAA 360  
303 GACCTCTCTGCTGGGTGGAGACCTGGGTTATCACTTCCAGCAAGACGTCCACTTCAAGGAA 362  
361 GAAACAGTGAAGCTTTATCTGTGAGCTGTGATGGCCCTGGACTACTGTCAGAACCCAG 420  
363 GAAACAGTGAAGCTTTATCTGTGAGCTGTGATGGCCCTGGACTACTGTCAGAACCCAG 422  
421 CGCATCATCTCAGAGGATGATGAAGCTGTCAATATTTTACTTTCAGCAACATGGGACGTTG 480  
423 CGCATCATCTCAGAGGATGATGAAGCTGTCAATATTTTACTTTCAGCAACATGGGACGTTG 482  
481 CACATCAGAGATTTCAACATTTCTGCGATGCTGCCAGGAGACACAGATTACCAACCATG 540  
483 CACATCAGAGATTTCAACATTTCTGCGATGCTGCCAGGAGACACAGATTACCAACCATG 542  
541 GTTGGCACCAGCCTTACATGGCACTGAGATGTTTCAAGTCTCAGAAAAGGACAGGCTAT 600  
543 GCTGGCACCAGCCTTACATGGCACTGAGATGTTTCAAGTCTCAGAAAAGGACAGGCTAT 602  
601 TCCTTTGCTGTTTCACTGTTGGTCCCTGGGAGTGCAGGCATATGAATGCTGTGAGAGCCGG 660

Copied from 10260845 on 08/11/2005

Db 603 TCCTTTCTGCTGACTGGTGGTCCCTGGAGTGAAGCATATGAACCTGCTGAGAGCGCG 662  
Qy 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACACGTTTGGAGACG 720  
Db 663 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACGTTTGGAGACG 722  
Qy 721 ACTGTTCTAACTTACCTTCTGCTGTCTCAGAGAAATGGTGTCACTTCTTAAAGGCTA 780  
Db 723 ACTGTTCTAACTTACCTTCTGCTGTCTCAGAGAAATGGTGTCACTTCTTAAAGGCTA 782  
Qy 781 CTCGAACCTAATCCAGACCAACGATTTTCTCAGTATCTGATGTCCAGAACTTCCCGTAT 840  
Db 783 CTCGAACCTAATCCAGACCAACGATTTTCTCAGTATCTGATGTCCAGAACTTCCCGTAT 842  
Qy 841 ATGAATGATATAAACTGGGATGCAATTTTTCAGAAAGGCTCATTCAGAGTTTCAATCCT 900  
Db 843 ATGAATGATATAAACTGGGATGCAATTTTTCAGAAAGGCTCATTCAGAGTTTCAATCCT 902  
Qy 901 AATAAGCGCAGGCTGAATTTGATCTCACTTTGAACTTGGAGAAATGATTTTGGAGTCC 960  
Db 903 AATAAGCGCAGGCTGAATTTGATCTCACTTTGAACTTGGAGAAATGATTTTGGAGTCC 962  
Qy 951 AAACCTCTACATAAGAAAAGGCTCTGCAAGAGGAGAGGATATCAGGAAATGC 1020  
Db 953 AAACCTCTACATAAGAAAAGGCTCTGCAAGAGGAGAGGATATCAGGAAATGC 1022  
Qy 1021 GATTCCTCTCAGACATGCTTCTTCAAGAGCACCTTGACTCTGTCCAGAGAGGATTCATA 1080  
Db 1023 GATTCCTCTCAGACATGCTTCTTCAAGAGCACCTTGACTCTGTCCAGAGAGGATTCATA 1082  
Qy 1031 ATTTTCAACAGAGAAAAGTAAACAGGACCTTTTAAACAAAGACAAACCAATCTAGCCTTG 1140  
Db 1033 ATTTTCAACAGAGAAAAGTAAACAGGACCTTTTAAACAAAGACAAACCAATCTAGCCTTG 1142  
Qy 1141 GAACAAACCAAGACCCCAAGTGCACAAATGGACAAATGGACA 1183  
Db 1143 GAACAAACCAAGACCCCAAGTGCAGATGATGGTCAAGATAACA 1185

RESULT 12  
US-10-108-260A-231  
; Sequence 231, Application US/10108260A  
; Publication No. US20040005560A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: NO. US20040005560A1e1 full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/10/108,260A  
; CURRENT FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 231  
; LENGTH: 2063  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-108-260A-231

Query Match 84.3%; Score 1032.2; DB 16; Length 2063;  
Best Local Similarity 99.7%; Pred. No. 3.9e-306;  
Matches 1034; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGGGAGCCAACTTCAAGAAAACCCAGGTGTTGATGAATAATGAAGATGTCAACTTT 60  
Db 334 ATGGGAGCCAACTTCAAGAAAACCCAGGTGTTGATGAATAATGAAGATGTCAACTTT 393  
Qy 61 GACCACTTTGAAATTTTGGGAGCCATGGGAAGCAGTTTTTGGGAAGGTCTGCATTGTA 120  
Db 394 GACCACTTTGAAATTTTGGGAGCCATGGGAAGCAGTTTTTGGGAAGGTCTGCATTGTA 453  
Qy 121 CAGAAAGATGATACCAAGAGATGTACGCAATGAAGTACATGAATAAACAAGAGTGGTG 180  
Db 454 CAGAAAGATGATACCAAGAGATGTACGCAATGAAGTACATGAATAAACAAGAGTGGTG 513

; PRIOR APPLICATION NUMBER: 09/560,875  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 09/496,914  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 2700  
; SOFTWARE: Custom  
; SEQ ID NO 239  
; LENGTH: 678  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-276-774-239

Query Match. 55.0%; Score 672.8; DB 13; Length 678;  
Best Local Similarity 99.7%; Pred. No. 7.4e-196; Indels 0; Gaps 0;  
Matches 674; Conservative 0; Mismatches 2;

QY 435 ATGAAGCCTGACAAATATTTTACTTGGACGAACATGGCAGCTGCACATCACAGATTTCAC 498  
Db 1 ATGAAGCCTGACAAATATTTTACTTGGACGAACATGGCAGCTGCACATCACAGATTTCAC 60  
QY 499 ATTCTCTGATGTGCCCAGGGAGACACAGATTACCCATGGCTGGCACCAGCCTTAC 558  
Db 61 ATTCTCTGATGTGCCCAGGGAGACACAGATTACCCATGGCTGGCACCAGCCTTAC 120  
QY 559 ATGCACCTGAGATGTTTCAGCTCCAGAAAGGAGCAGCTATTCTTCTGCTGTGACTGG 618  
Db 121 ATGCACCTGAGATGTTTCAGCTCCAGAAAGGAGCAGCTATTCTTCTGCTGTGACTGG 180  
QY 615 TGGTCCCTGGAGTGAGCGCATATGAATGCTGAGAGCCGAGACCGTATCATATTCCG 678  
Db 181 TGGTCCCTGGAGTGAGCGCATATGAATGCTGAGAGCCGAGACCGTATCATATTCCG 240  
QY 675 TCCAGTACTTCCAGCAAGAAATTTGTACACAGTTTGAGAGCAGCTGTTGTAACTTACCCT 738  
Db 241 TCCAGTACTTCCAGCAAGAAATTTGTACACAGTTTGAGAGCAGCTGTTGTAACTTACCCT 300  
QY 739 TCTGCCTGGTCCAGGAAATGGTCTCACTCTTAAAGCTACTCGAACCTAATCCAGAC 798  
Db 301 TCTGCCTGGTCCAGGAAATGGTCTCACTCTTAAAGCTACTCGAACCTAATCCAGAC 360  
QY 799 CAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTATATGAATGATATAAATCG 858  
Db 361 CAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTATATGAATGATATAAATCG 420  
QY 859 GATGAGTTTTTCAGAGAGCTCATTCAGGTTTCATTCCTAATAAGGAGCAGCTGAAT 918  
Db 421 GATGAGTTTTTCAGAGAGCTCATTCAGGTTTCATTCCTAATAAGGAGCAGCTGAAT 480  
QY 919 TGTGATCTTACCTTTTGAACCTTGAGAAATGATTTTGGAGTCCAAACCTCTACATAAGAA 978  
Db 481 TGTGATCTTACCTTTTGAACCTTGAGAAATGATTTTGGAGTCCAAACCTCTACATAAGAA 540  
QY 979 AAAAGCGCTCTGGCAAGAGAGGAGATATGAGAAATCGGATTTCTTCTCAGACATGT 1038  
Db 541 AAAAGCGCTCTGGCAAGAGAGGAGATATGAGAAATCGGATTTCTTCTCAGACATGT 600  
QY 1039 CTTCTTCAAGAGCCTTGTCTGTCAGAGAGGATTCATTAATTTTCAAAGAGAAAA 1098  
Db 601 CTTCTTCAAGAGCCTTGTCTGTCAGAGAGGATTCATTAATTTTCAAAGAGAAAA 660  
QY 1099 GTAAACAGGAGCTTTTA 1114  
Db 661 GTAAACAGGAGCTTTTA 676

RESULT 14  
US-09-841-683-6  
; Sequence 6, Application US/09841683  
; Patent No. US20020081600A1  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Yi  
; APPLICANT: Nepomnichy, Boris  
; APPLICANT: Wang, Xiaoming

QY 181 GAGCGCAATGAAGTGAGAAATGTTCTTCAAGGAATCCAGATATGCGAGGCTCGAGCAC 240  
Db 514 GAGCGCAATGAAGTGAGAAATGTTCTTCAAGGAATCCAGATATGCGAGGCTCGAGCAC 573  
QY 241 CCTTCTCTGTTAATTTTGTGTTATCTTCCAGATGAGGAGACATGTTTCAATGGTGGT 300  
Db 574 CCTTCTCTGTTAATTTTGTGTTATCTTCCAGATGAGGAGACATGTTTCAATGGTGGT 633  
QY 301 GACCTCTCTGCTGGTGGAGACCTGCTGTTATCACCTGCAACAGAACTGCTCAATTCAGAGAA 360  
Db 634 GACCTCTCTGCTGGTGGAGACCTGCTGTTATCACCTGCAACAGAACTGCTCAATTCAGAGAA 693  
QY 361 GAAACAGTGAAGCTCTTCAATCTGTGAGCTGTGATGCTGCGCCCTGGACTACCTCCAGAACCG 420  
Db 694 GAAACAGTGAAGCTCTTCAATCTGTGAGCTGTGATGCTGCGCCCTGGACTACCTCCAGAACCG 753  
QY 421 CGCATCTTCAAGGGATATGAAGCCTGACATATTTTACTTTGACGAACATGCGGACGCTG 480  
Db 754 CGCATCTTCAAGGGATATGAAGCCTGACATATTTTACTTTGACGAACATGCGGACGCTG 813  
QY 481 CACATCACAGATTTCAACATTTGCTGCGATGCTGCGCCAGGGAGACACAGATTACCAACCATG 540  
Db 814 CACATCACAGATTTCAACATTTGCTGCGATGCTGCGCCAGGGAGACACAGATTACCAACCATG 873  
QY 541 GCTGGCACCAAGCCTTACATGGCACTGAGATGTTTCACTCCAGAAAGGAGAGGCTAT 600  
Db 874 GCTGGCACCAAGCCTTACATGGCACTGAGATGTTTCACTCCAGAAAGGAGAGGCTAT 933  
QY 601 TCCCTTGTGTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
Db 934 TCCCTTGTGTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 993  
QY 661 AGACGATATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGTACACACGTTTGAGACG 720  
Db 994 AGACGATATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGTACACACGTTTGAGACG 1053  
QY 721 ACTGTTGTAACCTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
Db 1054 ACTGTTGTAACCTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1113  
QY 781 CTCGAACTTATCCAGACCAAGGATTTTCTCAGTTATCTGATGCTGCAAACTTCCCGTAT 840  
Db 1114 CTCGAACTTATCCAGACCAAGGATTTTCTCAGTTATCTGATGCTGCAAACTTCCCGTAT 1173  
QY 841 ATGAATGATATAAATCTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
Db 1174 ATGAATGATATAAATCTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1233  
QY 901 AATAAGCAGGCTGAATTTGTGATCTTACCTTTGAACCTTTGAGGAAATGATTTTGGAGTCC 960  
Db 1234 AATAAGCAGGCTGAATTTGTGATCTTACCTTTGAACCTTTGAGGAAATGATTTTGGAGTCC 1293  
QY 961 AAACCTCTACATAAGAAAGGCTGCTGCAAGAGAGGAGGATATGAGGAAATGC 1020  
Db 1294 AAACCTCTACATAAGAAAGGCTGCTGCAAGAGAGGAGGATATGAGGAAATGC 1353  
QY 1021 GATTCCTTCCAGACATG 1037  
Db 1354 GATTCCTTCCAGGTAAG 1370

RESULT 13  
US-10-276-774-239  
; Sequence 239, Application US/10276774  
; Publication No. US20040053245A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; APPLICANT: Tang, Y, Tom et al  
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-030  
; CURRENT APPLICATION NUMBER: US/10/276,774  
; CURRENT FILING DATE: 2002-11-18



```

US-09-841-683-4
; Sequence 4, Application US/09841683
; Patent No. US20020081600A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomniichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. US20020081600A1el Human Kinase Proteins and Polynucleotides Et
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 678
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-841-683-4

Query Match          53.9%; Score 660; DB 9; Length 678;
Best Local Similarity 100.0%; Pred. No. 6.4e-192; Indels 0; Gaps 0;
Matches 660; Conservative 0; Mismatches 0;

QY      1  ATGGGAGCCCAACACTTCAAGAAAACCCACGAGTGTGTGATGAATAAATGAAGATGTCAACTTT 60
DB      1  ATGGGAGCCCAACACTTCAAGAAAACCCACGAGTGTGTGATGAATAAATGAAGATGTCAACTTT 60

QY      61  GACCACTTTCAAAATTTTGGAGCCATTGGGAAGAGCAGTTTTTGGGAAGTCTGCAATTGTA 120
DB      61  GACCACTTTCAAAATTTTGGAGCCATTGGGAAGAGCAGTTTTTGGGAAGTCTGCAATTGTA 120

QY      121  CAGAAGAATGATACCAAGAAGATGTACGCAATGAAGTACATGAATAAACAAGAGTGC GTG 180
DB      121  CAGAAGAATGATACCAAGAAGATGTACGCAATGAAGTACATGAATAAACAAGAGTGC GTG 180

QY      181  GAGCGCAATGAAGTGAAGATGTCTTCAAGGAATCCAGATCATGACGGTCTGGAGCAC 240
DB      181  GAGCGCAATGAAGTGAAGATGTCTTCAAGGAATCCAGATCATGACGGTCTGGAGCAC 240

QY      241  CCYTTCCTGTTTAATTTGTGTATTTCCTTCCAAGATGAGGAAGACATGTTTCATGGTGTG 300
DB      241  CCYTTCCTGTTTAATTTGTGTATTTCCTTCCAAGATGAGGAAGACATGTTTCATGGTGTG 300

QY      301  GACCTCCTGCTGGGTGGAGACCTGCTGTTATCACTGTGCAACAGAA CGTCACTTCAGGAA 360
DB      301  GACCTCCTGCTGGGTGGAGACCTGCTGTTATCACTGTGCAACAGAA CGTCACTTCAGGAA 360

QY      361  GAAACGTGAAGCTTTCATCTGTGAGCTGGTTCATGGCCCTGCAGCTACCTGCGAAGACCAG 420
DB      361  GAAACGTGAAGCTTTCATCTGTGAGCTGGTTCATGGCCCTGCAGCTACCTGCGAAGACCAG 420

QY      421  CGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGA CGAA CATGGGCGAGTG 480
DB      421  CGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGA CGAA CATGGGCGAGTG 480

QY      481  CACATCACAGATTTCAACATTTGCTGCGATGCTGCCCGAGGAGACACAGATTACCAACATG 540
DB      481  CACATCACAGATTTCAACATTTGCTGCGATGCTGCCCGAGGAGACACAGATTACCAACATG 540

QY      541  GCTTGGCACCAAGCCCTTACATGGCACCTCAGATGTTTCAGTCCAGAAAAGAGCAGGCTAT 600
DB      541  GCTTGGCACCAAGCCCTTACATGGCACCTCAGATGTTTCAGTCCAGAAAAGAGCAGGCTAT 600

QY      601  TCCTTTGCTGTGTGACTGGTGTGCTTGGGAGTGA CGGCAATGTA ACTGCTGAGAGCGCG 660
DB      601  TCCTTTGCTGTGTGACTGGTGTGCTTGGGAGTGA CGGCAATGTA ACTGCTGAGAGCGCG 660

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Search completed: May 28, 2004, 09:36:31  
Job time : 593 secs

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OM nucleic - nucleic search, using sw model

Run on: May 28, 2004, 04:37:52 ; Search time 121 Seconds  
(without alignments)  
5613.718 Million cell updates/sec

Title: US-10-620-845-8  
Perfect score: 1224  
Sequence: 1 agggagccaaacttcaag.....agactctgaaggtttcataa 1224

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Sequences: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: /cgn2\_6/prodata/2/ina/5A\_COMB.seq.\*
  - 2: /cgn2\_6/prodata/2/ina/5B\_COMB.seq.\*
  - 3: /cgn2\_6/prodata/2/ina/6A\_COMB.seq.\*
  - 4: /cgn2\_6/prodata/2/ina/6B\_COMB.seq.\*
  - 5: /cgn2\_6/prodata/2/ina/PCFUS\_COMB.seq.\*
  - 6: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Rank	Score	Query Match	Length	ID	Description
1	1224	100.0	1224	US-09-841-683-8	Sequence 8, Appli
2	1224	100.0	1675	US-09-841-683-12	Sequence 12, Appli
3	1165.4	95.2	1191	US-09-841-683-10	Sequence 10, Appli
4	1160.6	94.8	1485	US-09-801-878B-1	Sequence 1, Appli
5	1160.6	94.8	1485	US-10-254-869-1	Sequence 1, Appli
6	661	54.0	711	US-09-841-683-6	Sequence 6, Appli
7	660	53.9	678	US-09-841-683-4	Sequence 4, Appli
8	484.8	39.6	1257	US-09-799-875-15	Sequence 15, Appli
9	484.8	39.6	1826	US-09-799-875-13	Sequence 13, Appli
10	470	38.4	1864	US-09-819-607-1	Sequence 1, Appli
11	181.8	14.9	148567	US-09-801-878B-3	Sequence 3, Appli
12	181.8	14.9	148567	US-10-254-869-3	Sequence 3, Appli
13	134.2	11.0	1008	US-09-394-455-3	Sequence 3, Appli
14	134.2	11.0	2549	US-09-467-082-3	Sequence 3, Appli
15	134.2	11.0	2549	US-09-394-455-5	Sequence 5, Appli
16	134.2	11.0	2608	US-09-394-455-35	Sequence 35, Appli
17	133.6	10.9	1619	US-09-394-455-14	Sequence 14, Appli
18	122.6	10.0	25603	US-09-819-607-3	Sequence 3, Appli
19	121.4	9.9	1788	US-09-417-197-68	Sequence 68, Appli
20	121.4	9.9	2211	US-09-394-455-39	Sequence 39, Appli
21	120.4	9.8	1498	US-09-509-902A-6	Sequence 6, Appli
22	120.4	9.8	1361	US-09-509-902A-15	Sequence 15, Appli
23	120.4	9.8	2204	US-08-221-817-12	Sequence 12, Appli
24	120.4	9.8	2204	US-08-454-439-12	Sequence 12, Appli
25	120.4	9.8	2204	US-09-841-683-12	Sequence 12, Appli
26	120.4	9.8	2206	US-08-221-817-10	Sequence 10, Appli
27	120.4	9.8	2206	US-08-454-439-10	Sequence 10, Appli

28 120.4 9.8 2206 5 PCT-US94-10487-10 Sequence 10, Appli  
29 120.4 9.8 2848 3 US-08-464-954A-2 Sequence 2, Appli  
30 120.4 9.8 5276 4 US-09-233-857-2 Sequence 2, Appli  
31 113 9.2 1599 3 US-09-256-465-1 Sequence 1, Appli  
32 113 9.2 1599 4 US-09-167-322-3 Sequence 3, Appli  
33 113 9.2 1599 4 US-09-023-655-1004 Sequence 1004, Ap  
34 110.8 9.1 1862 4 US-09-802-117-1 Sequence 1, Appli  
35 110.8 9.1 2249 4 US-09-802-117-5 Sequence 5, Appli  
36 110 9.0 2370 4 US-09-031-295-1 Sequence 1, Appli  
37 110 9.0 4438 4 US-09-566-921-81 Sequence 81, Appli  
38 109.8 9.0 2599 6 5266464-1 Patent No. 5266464  
39 109.2 8.9 1562 4 US-09-738-894A-1 Sequence 1, Appli  
40 109.2 8.9 1862 4 US-08-964-469-1 Sequence 1, Appli  
41 108.8 8.9 2754 3 US-09-429-322-3 Sequence 3, Appli  
42 106.8 8.7 2311 2 US-08-712-709-6 Sequence 6, Appli  
43 106.8 8.7 2311 3 US-09-111-444-6 Sequence 6, Appli  
44 106.8 8.7 2311 3 US-09-541-228-6 Sequence 6, Appli  
45 106.8 8.7 2311 4 US-09-016-434-772 Sequence 772, App

ALIGNMENTS

RESULT 1  
US-09-841-683-8  
; Sequence 8, Application US/09841683  
; Patent No. 6617147  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Yi  
; APPLICANT: Nepomichy, Boris  
; APPLICANT: Wang, Xiaoming  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Scoville, John  
; APPLICANT: Walke, D. Wade  
; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding t  
; FILE REFERENCE: LEX-0167-USA  
; CURRENT APPLICATION NUMBER: US/09/841,683  
; PRIOR FILING DATE: 2001-04-24  
; PRIOR APPLICATION NUMBER: US 60/199,499  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: US 60/201,227  
; PRIOR FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1224  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-841-683-8

Query Match 100.0%; Score 1224; DB 4; Length 1224;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGAGCCAACTTCAAGAAACCCAGCTGTGATGAAATGAAGATGTCACATTT 60  
DB 1 ATGGGAGCCAACTTCAAGAAACCCAGCTGTGATGAAATGAAGATGTCACATTT 60  
QY 61 GACCACTTTGAAATTTTCGAGCCATTCGGAAGGAGCTTTTGGGAAGGCTCTGCATTGTA 120  
DB 61 GACCACTTTGAAATTTTCGAGCCATTCGGAAGGAGCTTTTGGGAAGGCTCTGCATTGTA 120  
QY 121 CAGAAAGATGATPACCAAGAGATGTACCAATGAAGTACATGAATPAAACAAAGTGGCGTG 180  
DB 121 CAGAAAGATGATPACCAAGAGATGTACCAATGAAGTACATGAATPAAACAAAGTGGCGTG 180  
QY 181 GAGCCCAATGAGTGAAGAAATGCTTCAAGAACTCCAGATCATCGAGGCTTGAGCAC 240  
DB 181 GAGCCCAATGAGTGAAGAAATGCTTCAAGAACTCCAGATCATCGAGGCTTGAGCAC 240  
QY 241 CCTTTCTCGGTTAAATTTCTGTTGTTATTCCTTCCAAGATGAGGAAGACATGTTTCATGTTGGTG 300  
DB 241 CCTTTCTCGGTTAAATTTCTGTTGTTATTCCTTCCAAGATGAGGAAGACATGTTTCATGTTGGTG 300

Query Match	100.0%;	Score 1224;	DB 4;	Length 1675;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1224;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
1	ATGGGAGCCAACTTCCAAAGAAACCCACAGTGTGTTGATGAATAATGAAGATGTCAACTTT	60		
4:3	ATGGGAGCCAACTTCCAAAGAAACCCACAGTGTGTTGATGAATAATGAAGATGTCAACTTT	472		
61	GACCACCTTTGAAATTTTTCGCGAGCCATTTCGGGAAAGCGCAGTTTTCGGGAAAGTCTGCAATTTGA	120		
473	GACCACCTTTGAAATTTTTCGCGAGCCATTTCGGGAAAGCGCAGTTTTCGGGAAAGTCTGCAATTTGA	532		
121	CAGAAGAATGATCCAGAAGATGTACCAATGAAGTACATGAATAAACAAGAGTCGCTG	180		
533	CAGAAGAATGATCCAGAAGATGTACCAATGAAGTACATGAATAAACAAGAGTCGCTG	592		
181	GAGCGCAATGAAGTGAGAAATGTCTTCAAGAACTCCAGATCATCGAGGTCCTGAGCAC	240		
593	GAGCGCAATGAAGTGAGAAATGTCTTCAAGAACTCCAGATCATCGAGGTCCTGAGCAC	652		
241	CCTTTCCTGGTTAAATTTGTGTTATTCCTTCCAAGATGAGGAAGCATGTTTCATGGTGGTG	300		
653	CCTTTCCTGGTTAAATTTGTGTTATTCCTTCCAAGATGAGGAAGCATGTTTCATGGTGGTG	712		
301	GACCTCCTGCTGGGTGGAGACCTGGTTATCACCTGCAACAGAGCTCCACTTCAAGAA	360		
7:3	GACCTCCTGCTGGGTGGAGACCTGGTTATCACCTGCAACAGAGCTCCACTTCAAGAA	772		
361	GAACAGTGAAGCTCTTTCATCTGTGAGCTGTCTATGGCCCTGGACTACTCGCAGAACACAG	420		
773	GAACAGTGAAGCTCTTTCATCTGTGAGCTGTCTATGGCCCTGGACTACTCGCAGAACACAG	832		
421	CGCATCATTCACGGGATATGAAGCCTGACAAATATTTTACTTGAACGAATCGGGCACGTG	480		
833	CGCATCATTCACGGGATATGAAGCCTGACAAATATTTTACTTGAACGAATCGGGCACGTG	892		
481	CACATCACAGATTTTCACATTTGCTGCGATGCTGCCAGGGAGACACAGATTACCACCATG	540		
893	CACATCACAGATTTTCACATTTGCTGCGATGCTGCCAGGGAGACACAGATTACCACCATG	952		
541	GCTGGCCAAAGCCTTACATGGCACCTTGAGATGTTTCAGCTCCAGAAAGGAGCAGGCTAT	600		
953	GCTGGCCAAAGCCTTACATGGCACCTTGAGATGTTTCAGCTCCAGAAAGGAGCAGGCTAT	1012		
601	TCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGAACGATATGAATCTGCTGAGAGGCCGG	660		
1013	TCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGAACGATATGAATCTGCTGAGAGGCCGG	1072		
661	AGACGGTATCATATTCGCTCCAGTACTTCCAGCAAGGAATTTGACACAGCTTTGAGACG	720		
1073	AGACGGTATCATATTCGCTCCAGTACTTCCAGCAAGGAATTTGACACAGCTTTGAGACG	1132		
721	ACTGTGTAACTTACCCTTCTGCTGGTTCACAGGAATTTGGTGTCACTTCTTAAAAAGCTA	780		

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Copied from 10260845 on 08/11/2005



```

; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding t
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 711
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-841-683-6

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Query Match      54.0%; Score 661; DB 4; Length 711;
Best Local Similarity 100.0%; Pred. No. 5.7e-196;
Matches 661; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1	ATGGAGCCAACTTCTCAAGAAAACCAACAGTGTGTTGATGAAATGAGATGTCAACTTT	60
1	ATGGAGCCAACTTCTCAAGAAAACCAACAGTGTGTTGATGAAATGAGATGTCAACTTT	60
61	GACCACATTTGAAATTTTGGCGAGCATTTGGGAAGGCGATTTTGGGAAGCTCTGCATTGTA	120
61	GACCATTTTGAATTTTGGAGCCATTGGGAAAGGCGAGTTTGGGAAAGTCTGCATTGTA	120
121	CAGAAGATGATACCAAGAAGATGTACGCAATGAAGTACATGAATPAAACAAAGTGCGTG	180
121	CAGAAGATGATACCAAGAAGATGTACGCAATGAAGTACATGAATPAAACAAAGTGCGTG	180
181	GAGCGCAATGAAGTGAAGAATGTTCTTCAAGGAACTCCAGATCATCGAGGCTCTGGAGCAC	240
181	GAGCGCAATGAAGTGAAGAATGTTCTTCAAGGAACTCCAGATCATCGAGGCTCTGGAGCAC	240
241	CTTTTCTCGTTAAATTTGTGTAATTCCTTCCAAGATGAGGAAGACATGTTCATGTGGTG	300
241	CTTTTCTCGTTAAATTTGTGTAATTCCTTCCAAGATGAGGAAGACATGTTCATGTGGTG	300
301	GACCTCTGCTGGTGGAGACCTGGTTATCACTTGCACAGAAAGTCCCACTTCAAGAA	360
301	GACCTCTGCTGGTGGAGACCTGGTTATCACTTGCACAGAAAGTCCCACTTCAAGAA	360
361	GAAACAGTGAAGCTTTCATCTGTGAGCTGTGTCATGGCCCTGGACTACTCTGCAGAACAG	420
361	GAAACAGTGAAGCTTTCATCTGTGAGCTGTGTCATGGCCCTGGACTACTCTGCAGAACAG	420
421	CGCATCATTTACAGGGATATGAAGCCTGACATATTTACTTGACGAACATGGGCACGTG	480
421	CGCATCATTTACAGGGATATGAAGCCTGACATATTTACTTGACGAACATGGGCACGTG	480
481	CACATCACAGATTTCAACATTTGCTGCGATGCTGCCCGGGAGACACAGATTACACCATG	540
481	CACATCACAGATTTCAACATTTGCTGCGATGCTGCCCGGGAGACACAGATTACACCATG	540
541	GCTGGCACCAAGCCTTACATGGGCACTTGAGATGTTCAGCTCCAGAAAAAGGACGGCTAT	600
541	GCTGGCACCAAGCCTTACATGGGCACTTGAGATGTTCAGCTCCAGAAAAAGGACGGCTAT	600
601	TCCTTTGCTGTTACATGGTGGTCCCTGGGAGTGAAGGATATGAATCTGCTGAGAGGCCGG	660
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661	A	661
661	A	661

RESULT 6  
US-09-841-683-6  
; Sequence 6, Application US/09841683  
; Patent No. 6617147  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Yi  
; APPLICANT: Nepomnichy, Boris

## RESULT 6



RESULT 7  
 US-09-841-683-4  
 ; Sequence 4, Application US/09841683  
 ; Patent No. 6617147  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nepomnichy, Boris  
 ; APPLICANT: Hu, Yi  
 ; APPLICANT: Wang, Xiaoming  
 ; APPLICANT: Doncho, Gregory  
 ; APPLICANT: Scoville, John  
 ; APPLICANT: Walke, D. Wade  
 ; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding  
 ; FILE REFERENCE: LEX-0167-USA  
 ; CURRENT APPLICATION NUMBER: US/09/841,683  
 ; CURRENT FILING DATE: 2001-04-24  
 ; PRIOR APPLICATION NUMBER: US 60/199,499  
 ; PRIOR FILING DATE: 2000-04-25  
 ; PRIOR APPLICATION NUMBER: US 60/201,227  
 ; PRIOR FILING DATE: 2000-05-01  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 678  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 ; US-09-841-683-4  
 Query Match 53.9%; Score 660; DB 4; Length 678;  
 Best Local Similarity 100.0%; Pred. No. 1.le-195;  
 Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 ATGGAGGCAACACCTTCAAGAAACACACAGTGTGTTGATGAAATGAAGATGTCAACTTT 60  
 1 ATGGAGGCAACACCTTCAAGAAACACACAGTGTGTTGATGAAATGAAGATGTCAACTTT 60  
 61 GACCACTTTGAAATTTTCGAGCCATTGGGAAAGGACGTTTTGGGAAGGTTCTGCAATTGA 120  
 61 GACCACTTTGAAATTTTCGAGCCATTGGGAAAGGACGTTTTGGGAAGGTTCTGCAATTGA 120  
 121 CAGAGAGATGATACCAAGAGATGATGACCAATGATGATGATGATGATGATGATGATGATG 180  
 121 CAGAGAGATGATACCAAGAGATGATGACCAATGATGATGATGATGATGATGATGATGATG 180  
 181 GAGCGCAATGAAGTGAGAAATGCTCTTCAAGGAATCTCCAGATCATCGAGGCTCTGAGCAC 240  
 181 GAGCGCAATGAAGTGAGAAATGCTCTTCAAGGAATCTCCAGATCATCGAGGCTCTGAGCAC 240  
 241 CCTTCTCTGTTAATTTGTTGTTATCTTCCAGATGAGGAAGACATGTTTCAATGTTGTTG 300  
 241 CCTTCTCTGTTAATTTGTTGTTATCTTCCAGATGAGGAAGACATGTTTCAATGTTGTTG 300  
 301 GACCTCTCTGTTGTTGAGAGCTGCTGTTATCACCCTGACAGAGAGTCCATTCAGGA 360  
 301 GACCTCTCTGTTGTTGAGAGCTGCTGTTATCACCCTGACAGAGAGTCCATTCAGGA 360  
 361 GAAACAGTGAAGCTTCTCATCTGTGAGCTGTCTATGCTGCTGCTGCTGCTGCTGCTGCTG 420  
 361 GAAACAGTGAAGCTTCTCATCTGTGAGCTGTCTATGCTGCTGCTGCTGCTGCTGCTGCTG 420  
 421 CGCATCTTCAGGATATGAGAGCTGACAAATATTTTACTGTGAGAAATGAGGACGCTG 480  
 421 CGCATCTTCAGGATATGAGAGCTGACAAATATTTTACTGTGAGAAATGAGGACGCTG 480  
 481 CACATCAGATTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
 481 CACATCAGATTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
 541 GCTGCAACAGGCTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
 541 GCTGCAACAGGCTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
 601 TCCCTTGTGTTGATGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660

Db 601 TCCCTTGTGTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
 RESULT 8  
 US-09-799-875-15  
 ; Sequence 15, Application US/09799875  
 ; Patent No. 6638721  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Meyers, Rachel  
 ; APPLICANT: Kapeller-Libermann, Rosana  
 ; APPLICANT: Williamson, Mark  
 ; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses  
 ; FILE REFERENCE: 35800/209996  
 ; CURRENT APPLICATION NUMBER: US/09/799,875  
 ; CURRENT FILING DATE: 2001-03-06  
 ; PRIOR APPLICATION NUMBER: 60/182,059  
 ; PRIOR FILING DATE: 2000-02-11  
 ; PRIOR APPLICATION NUMBER: 09/659,287  
 ; PRIOR FILING DATE: 2000-09-12  
 ; NUMBER OF SEQ ID NOS: 32  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 15  
 ; LENGTH: 1257  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-799-875-15  
 Query Match 39.6%; Score 484.8; DB 4; Length 1257;  
 Best Local Similarity 66.7%; Pred. No. 7.7e-141;  
 Matches 728; Conservative 0; Mismatches 352; Indels 12; Gaps 2;  
 QY 28 CCAGTGTGTTGATGAAATGAAGATGTCAACTTTGACCACTTTGAAATTTTCGAGCCATT 87  
 Db 37 CCAGTGTGTTGACCAAGAGGACGTGAATTCACCACTTCAGATCCCTTCGGGCCATT 96  
 QY 38 CGGAAGGACGATTTGGGAAGTCTGCAATTCAGAAAGATGATACCAAGAGATGTAC 147  
 Db 37 GGGAGGCGCAGTTTGGCAGGTGTGCAATTCAGAAAGCGGACACGGAGAGATGTAC 156  
 QY 148 GCAATGAAGTACATGAATAAACAAGAGTGTGCTGAGCGCAATGAAGTGAAGAAATGTCTTC 207  
 Db 157 GCCATGAAGTACATGAACAGCAGCAGTGCATCAGCGCGACGAGGTCCGCAAGCTCTTC 216  
 QY 208 AAGCACTCCAGATCATGACGGTCTGAGCACCCTTCTGCTGTTAATTTGCTGATTC 267  
 Db 217 CGGAGCTGGAGATCTCTGAGGAGATCGAGCAGCTTCTGCTGTTAATTTGCTGATTC 276  
 QY 258 TTCAAGATGAGGAAGACATGTTTCAATGTTGTTGACCTCTCTGCTGTTGAGACCTTCGCT 327  
 Db 277 TTCCAGAGCAGGAGGACATGTTTCAATGTTGTTGACCTCTCTGCTGTTGAGACCTTCGCT 336  
 QY 328 TATCACTGCAACAGAGCTCCACTTCAAGGAAGAAACAGTGAAGCTCTTCATCTGTGAG 387  
 Db 337 TACCACCTGACGAGAACGTCAGTCTTCCAGAGACACGCTGAGGCTGTATCATCTGGAG 396  
 QY 388 CTGTCTATGSCCTTGGACTCTCAGAACACAGCGCATCATTCACAGGATATGAAGCT 447  
 Db 397 ATGSCATCTGCTTGGACTCTCTGCGGCGCAGCAGCATCATTCACAGATGTCAAGCT 456  
 QY 448 GACAATATTTTACTTGAACACATGGGCACTGTCATCATCAGATTTCAACATTTGCTGCG 507  
 Db 457 GACAACATTTCTCTGATGAGAGGACATGCACCTGACCGACTTCAACATTTGCCACC 516  
 QY 508 ATGCTGCCAGGAGACACAGATTAACAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 567  
 Db 517 ATCATCAAGACCGGAGCGGCGGCGCATTTAGAGGACACCAAGCGCTATCATGCTGCG 576  
 QY 568 GAGATGTTTCACTC-----CAGAAAGGAGCGGCTATTTCTTGTGCTGTTGCTGCTG 621  
 Db 577 GAGATCTTCACTCTTTTGTCAACGGCGGACCGGCTATCTCTTCGAGGTGAGCTGCTG 636  
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Db 637 TCCTGGGGGATGATGCCCTATGAGTGCCTGCGAGGATGAGGCCCTATGACATCCACTCC 696
Qy 682 AGTACTTCCAGCAAGGAAATTTGACACAGTTTGGACGACACTGTGTAACTTACCCCTCT 741
Db 697 AGCAACGCGTGGAGTCCCTGGTGCAGTGTTCAGCACCGTGAGCTCCAGTATGTCCCC 756
Qy 742 GCGTGTGACAGAAATGTTGTCATCTTTTAAAGCTACTGAACTTAATCCAGACCAA 801
Db 757 AGCTGCTCAAGAGATGTTGCTTGGTGGGAAAGCTCTCACTGTGAACCCGAGCAC 816
Qy 802 CGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTATATGATATATAAATCTGGAT 861
Db 817 CGGCTCTCCAGGCTCCAGGAGTGCAGGAGGAGCCCGCGCTGCGGCGCTGTGTGGAC 876
Qy 862 GCAGTTTTCAGAGAGGCTCATCTCCAGGTTTCATTCCTTAATAAGGCGAGGCTGAATCT 921
Db 877 CACCTGAGCGAGAGAGGTTGGAGCGGGCTTCGTGCCCAACAAAGGCGCTGTGCACTGC 936
Qy 922 GATCTTACCTTTGAACTTGAGGAAATGATTTTGGAGTCCAAACCTCTACATAAGAAAAA 981
Db 937 GACCCACACCTTTGAGCTGGAGAGATGATCTCTGGAGTCCAGGCCCTGCAAGAAGAG 996
Qy 982 AAGCTCTGCGAAGAGCA-----GAAGGATATGAGGAATGCGATTTCTTCTAGACA 1035
Db 997 AAGCGTCTGGCAAGAAAGTCCCGGGAACAAGTCCCGGGAACAAGAGGAGCTCCAGTCCG 1056
Qy 1036 TGTCTTCTTCAAGAGCACCTTGACTCTGTCAGAGGAGTTCATATTTTCAACAGAGAA 1095
Db 1057 GACTATCTTCAAGAGCTGCTCGATGCCATCCAGCAGAGACTTGTGTATTTTACAGAGA 1116
Qy 1096 AAGTAAACAGG 1107
Db 1117 AAGCTGAAGAGG 1128

Query Match 39.6%; Score 484.8; DB 4; Length 1826;
Best Local Similarity 66.7%; Pred. No. 9.9e-141;
Matches 728; Conservative 0; Mismatches 352; Indels 12; Gaps 2;

Qy 28 CCAGTGTTCATGAAATGAAGATGTCACCTTTGACCACTTTTGAAATTTTGGCAGCCATT 87
Db 53 CCGGTGTTTGACGACAGGAGGAGTGAAGTTCGACCACTTCAGATCTCTCGGCGCAT 112
Qy 88 GGGAAAGGCGAGTTTGGGAGGTTCTGCAATTTGTACAGAGATGATACCAAGAGATGTAC 147

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RESULT 10

US-09-819-607-1  
; Sequence 1, Application US/09819607  
; Patent No. 6686176  
; GENERAL INFORMATION:  
; APPLICANT: BEASLEY, Ellen et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001078  
; CURRENT APPLICATION NUMBER: US/09/819,607  
; CURRENT FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1864  
; TYPE: DNA  
; ORGANISM: Human  
; US-09-819-607-1

Query Match 38.4%; Score 470; DB 4; Length 1864;  
Best Local Similarity 66.1%; Pred. No. 4.2e-136;  
Matches 715; Conservative 0; Mismatches 355; Indels 12; Gaps 2;

38 ATGAAATGAGATGTCACACTTTCGACCACTTTGAAATTTTCGAGCCATTGGGAAAGSCA 97  
89 AAGCAGAGAGCGAGTGAATTCGACCACTTCCAGATCTTCGGGGCATTGGGAAAGSCA 148  
98 GTTTTGGAGGCTCTGCAATTTACAGAGATGATACCAAGAGATGTACGCAATGAAGT 157  
149 GCTTTGGCAAGGTGTGATCTGTGAGAGCGGACCGAGAGATGTACGCCATGAAGT 208  
158 ACATGAATTAACAAAGTGTGAGGCGCATGAAGTGAAGTGAAGTGTCTTCAGGAATCTCC 217  
209 ACATGAATTAACAAAGTGTGAGGCGCATGAAGTGAAGTGAAGTGTCTTCAGGAATCTCC 268  
218 AGATCATGACGGGTCTGAGCAGCACCCTTTCCTGCTTAAATTTGCTGATTTCTTCCAAAGT 277  
269 AGATCTTCAGGAGATGAGCAGCCTTCTCTGCTGAGACCTCTGATCTCTTCAGGAGCG 328  
278 AGGAGACATGTTTCATGCTGTGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 337  
329 AGGAGACATGTTTCATGCTGTGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 388  
338 AACAGACGTCCTTCAAG 397  
389 AGCAGACGTCGAGTTTCCGAGGACACGCTGAGGCTGTACATCTGCGAGATGCGACTGG 448  
398 CCTGGAATCTCTGAG 457  
449 CTCTGGAATCTCTGAG 508  
458 TACTTGAG 517  
509 TCCTGAGATGAG 568  
518 GGGAGACAGATTAACCATGCTGCGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 577  
569 ACGGGAG 628  
578 GCTC-----CAGAAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 631  
629 ACTCTTTTGTCAAGGGGGGAG 688  
632 TGACGGATATGAGATCTGAG 691  
689 TGATGGGCTATGAGTGTGAG 748  
692 GCAAGGAATATGATACACAGCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 751  
749 TGGAGTCCCTGCTGAGTGTTCAGACCGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 808  
752 AGGAAATGGTGTCACTTCTTAAAGAGTACTTCGAAACCTTAATCCAGACCAACGATTTTCTC 811

Db 809 AGGAGATGGTGGCTTCTCTCGGAGAGCTCTCTCACTGTGAACCCCGAGACCGGGCTCTCCA 868  
Qy 8.2 AGTTATCTGATGTCCAGAACTTCCCGTATATGATATGATATAAACTGGGATGCACTTTTTC 871  
Db 869 GCCTCCAGAGAGCTGCAGGAGCCCGCGCTGGCGGCTGTGTGGGACCCACCTGAGCG 928  
Qy 8.2 AGAAGAGCTCATTCAGGTTTCATTCCTTAATAAGGAGCGCTGAATTTGATCTTACCT 931  
Db 929 AGAAGAGGTTGGAGCGCGGCTTCTGTGCCCAACAAGAGCGCTCTGCACTGGGACCCACCT 988  
Qy 932 TTGAACCTTGAGGAAATGATTTTGGAGTCCAAACCTCTACATTAAGAAAAAAGCGTCTGG 991  
Db 989 TTGAGCTGGAGAGATGATCTGTGGAGTCCAGGCCCTTCGACAGAGAGAGAGCGCTGG 1048  
Qy 992 CAAAGAAAGGA-----GAAGGATATGAGAAATTCGATTTCTTCTCAGACATGTCTTCTTC 1045  
Db 1049 CCAAGAACAAAGTCCCGGCAACAAGAGAGAGAGCTCCAGTCCGAGATGACTATCTTC 1108  
Qy 1046 AAGAGCACTTGACTCTGTCCAGAGAGAGTTCATATTTTCAACAGAGAAAAAGTAAACA 1105  
Db 1109 AAGACTGCTCGATGTCATCCAGCAAGACTTCGTGATTTTAAACAGAGAAAAAGCTGAAGA 1168  
Qy 1106 GG 1107  
Db 1169 GG 1170

RESULT 11  
US-09-801-876B-3  
; Sequence 3, Application US/09801876B  
; Patent No. 6492155  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001160  
; CURRENT APPLICATION NUMBER: US/09/801,876B  
; CURRENT FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 148567  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(148567)  
; OTHER INFORMATION: n = A, T, C or G  
US-09-801-876B-3

Query Match 14.9%; Score 181.8; DB 4; Length 148567;  
Best Local Similarity 89.9%; Pred. No. 6.2e-45;  
Matches 195; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 252 TAATTTGTTGTTATTCCTTCCAGATGAGAGAGATGTTTCATGTTGGTGGACCTCTCTGCT 311  
Db 86036 TAATTCAGGTATTCCTTCCAGATGAGAGAGATGTTTCATGTTGGTGGACCTCTCTGCT 86095  
Qy 312 GGGTGGAGAGCTCGTTATTCACCTGCAACAGAGAGCTCCACTTCAAGAGAAAAAGTGA 371  
Db 86096 GGGTGGAGAGCTCGTTATTCACCTGCAACAGAGAGCTCCACTTCAAGAGAAAAAGTGA 86155  
Qy 372 GCTCTTTTCATGTGAGCTGTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 431  
Db 86156 GCTCTTTTCATGTGAGCTGTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 86215  
Qy 432 CAGGAGATGAGAGCTGTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 468  
Db 86216 CAGGTCAGTCAAGTCCAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 86252

RESULT 12

US-10-254-869-3

Sequence 3, Application US/10254869

Patent No. 653117

GENERAL INFORMATION:

APPLICANT: YE, Jane et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL001160DIV

CURRENT APPLICATION NUMBER: US/10/254,869

CURRENT FILING DATE: 2002-09-26

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 148567

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (1)...(148567)

OTHER INFORMATION: n = A,T,C or G

US-10-254-869-3

Query Match

Best Local Similarity 14.9%; Score 181.8; DB 4; Length 148567;

Mismatches 195; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

252 TAAATTTGGTATTCCTTCCAGATGAGGAGACATGTTTCATGTTGGTGGACCTCCTGCT 311

86036 TAAATCCAGGTATTCCTTCCAGATGAGGAGACATGTTTCATGTTGGTGGACCTCCTGCT 86095

312 GGGTGGAGACCTGGTTATACCTGCGACAGAAAGTCCATTCCTCAAGAGAAACAGTGAA 371

86096 GGGTGGAGACCTGGTTATACCTGCGACAGAAAGTCCATTCCTCAAGAGAAACAGTGAA 86155

372 GCTCTTCATCTGTCAGCTGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 431

86156 GCTCTTCATCTGTCAGCTGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 86215

432 CAGGAGATGAAGCTGCATATATTTACTTGACGAA 468

86216 CAGTCACTCAAGTCCAGGAGATGGCCATCAACGTA 86252

RESULT 13

US-09-394-455-3

Sequence 3, Application US/09394455

Patent No. 6531305

GENERAL INFORMATION:

APPLICANT: Witman, George F.

APPLICANT: San Agustín, Jovenal

APPLICANT: Leszyk, John D.

TITLE OF INVENTION: SPERM ASSOCIATED PROTEIN KINASE POLYPEPTIDES, CORRESPONDING

TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USE

FILE REFERENCE: 07917/078001

CURRENT APPLICATION NUMBER: US/09/394,455

CURRENT FILING DATE: 1999-09-10

PRIOR APPLICATION NUMBER: US 60/099,771

PRIOR FILING DATE: 1998-09-10

NUMBER OF SEQ ID NOS: 56

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 1008

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(1008)

US-09-394-455-3

Query Match

Best Local Similarity 11.0%; Score 134.2; DB 4; Length 1008;

Mismatches 324; Conservative 0; Mismatches 256; Indels 15; Gaps 2;

Qy 52 GTCACTTTGACCACTTTGAAATTTTCGAGCCATTCGGAAAGCAGTTTGGGAAGTC 111

Db 70 GCCCATTGGATCAGTTTGAACGAATCAAGACCCCTCGGCACGGGCTCCTTCGGCGGGTG 129

Qy 112 TGCATTCTCAGAGATGATACCAAGAAATGTACCAATCAAGTCAATCAATCAATCAAA 171

Db 130 ATGCTGTGAAACCAAGGAGACCGGAAACCACTATGCCATGAAGATCCTCGCAAAACAG 189

Qy 172 AAGTGCCTGAGCGCAATGAAGTGAAGAAATGTCTTCAAGGAATCCAGATCATGACAGGT 231

Db 190 AAGTGTGAAACCTGAACACAGATCGAACACACCTGATGAAGCGCATCTCTGCAAGCT 249

Qy 232 CTGGAGCACCTTCTCTGTTTAAATTTGTGTTTCTTCCAAAGATGAGGAAGATGTTTC 291

Db 250 GTCAACTTTCCTCTCGTCAAACTCGAGTTCTCTTCAAGGACAACTCAAACTTATAC 309

Qy 292 ATGCTGTGACCTCTCTGCTGGTGGAGACCTGCTTATCACCTGCAACAGAACTCCAC 351

Db 310 ATGCTCATGAGTACGTGCGCGCGGAGATGTTCTCACACCTACGCGGATCGGAAGG 369

Qy 352 TTCAAGGAAGAAACAGTGAAGCTCTTCATCTGTGAGCTGTGCTGCTGCTGCTGCTGCTG 411

Db 370 TTCACTGAGCCCATGCGCGTTTCTACGCGGCCAGATCGTCTGACCTTTGAGTATCTG 429

Qy 412 CAGAACCCAGCGCATCATCAAGGATATGAAGCTGCAATATTTTACTTTGAGCAAACT 471

Db 430 CACTCGCTGGATCTCATCTACAGGACCTGAAGCGGAGATCTGCTCAATTGACCCAGCAG 489

Qy 472 GGGCACCTGCACATCACAGATTTCAACATTCCTGCGATGCTGCCAGGAGACACAGATT 531

Db 490 GGTACATTCAGGTGACAGACTTCGGTTTCGCAA-----GCGGTGAAGGGCGGACT 543

Qy 532 ACCACCATGGCTGGCACCAAGCCCTTACATGCGCACTGAGATGTTTCAAGTCCAGAAAAGGA 591

Db 544 TGGACCTTGTGCGCACCCCTGAGTACTTGGCCCTGAGATTATCTTGAGCAA----- 596

Qy 592 CGAGCTATTCCTTTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 648

Db 597 --AGGCTACAAAGGCGGTGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 651

RESULT 14

US-09-467-082-3

Sequence 3, Application US/09467082

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Lex M. Cowser

TITLE OF INVENTION: ANTISENSE MODULATION OF PKA CATALYTIC SUBUNIT C-ALPHA EXPRESSION

FILE REFERENCE: RYS-0086

CURRENT APPLICATION NUMBER: US/09/467,082

CURRENT FILING DATE: 1999-12-17

NUMBER OF SEQ ID NOS: 49

SEQ ID NO 3

LENGTH: 2549

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (81)...(1136)

NAME/KEY: unsure

LOCATION: 6

OTHER INFORMATION: unknown

US-09-467-082-3

Query Match

Best Local Similarity 11.0%; Score 134.2; DB 3; Length 2549;

Mismatches 324; Conservative 0; Mismatches 258; Indels 15; Gaps 2;

Qy 52 GTCACTTTGACCACTTTGAAATTTTCGAGCCATTCGGAAAGCAGTTTGGGAAGTC 111

Db 195 GCCCATTGGATCAGTTTGAACGAATCAAGACCCCTCGGCACGGGCTCCTTCGGCGGGTG 254

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Qy 112 TGCATTGTACAGAGAGATGATACCAAGAGATGTACGCAATGATGAAGTACATCAATTAACAA 171
Db 255 ATGCTGTGTGAACACACAGAGAGACCGGGAACCACTATGCCATGAAGATCCTCGACAAACAG 314
Qy 172 AAGTGCCTGGAGCGCAATGAAGTGAAGATGTCTTCAAGGAACCTCCAGATCATGCGGCT 231
Db 315 AAGTGTGTGAACACACAGAGATGAAACACACACACACACACACACACACACACACACAC 374
Qy 232 CTGGAGACACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 291
Db 375 GTCAACTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 434
Qy 292 ATGCTGTGTGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 351
Db 435 ATGCTGTGTGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 494
Qy 352 TTCAAGGAAGAAACAGTGAAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 411
Db 495 TTCAAGGAAGAAACAGTGAAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 554
Qy 412 CAGAACACAGCGCATCATTCACAGGAGATGAAGCTGCAATATTTTACTTTGACGAACAT 471
Db 555 CACTCGCTGATCTCATTCACAGGAGCTGAAGCGGAGATCTGCTCATTTGACCGACAG 614
Qy 472 GGGCAGCTGCACATCACAGATTTCAACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 531
Db 615 GGCTACATCAGTGAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668
Qy 532 ACCACATGCTGGCACCACCAAGCTTACATGACCTGAGATGTTGAGTCTCCAGAAAGGA 591
Db 669 TGGACCTTGTGCGGACCCCTGAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 721
Qy 592 GCAGGCTATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 648
Db 722 --AGGCTACAAAGGCGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 776

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PSLT 15

US-09-394-455-5

Sequence 5, Application US/09394455

Patent No. 6531305

GENERAL INFORMATION:

APPLICANT: Witman, George F.

APPLICANT: San Agustín, Jovenal

APPLICANT: Leszyk, John D.

TITLE OF INVENTION: SPERM ASSOCIATED PROTEIN KINASE POLYPEPTIDES, CORRESPONDING

TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USE

FILE REFERENCE: 07917/078001

CURRENT APPLICATION NUMBER: US/09/394,455

PRIOR FILING DATE: 1999-09-10

PRIOR FILING DATE: 1998-09-10

NUMBER OF SEQ ID NOS: 56

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 2549

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (81)...(1133)

NAME/KEY: misc\_feature

LOCATION: (1)...(2549)

OTHER INFORMATION: n = A,T,C or G

US-09-394-455-5

Query Match 11.0%; Score 134.2; DB 4; Length 2549;

Best Local Similarity 54.3%; Pred.No.2.9e-31;

Matches 324; Conservative 0; Mismatches 259; Indels 15; Gaps 2;

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Qy 52 GTCACCTTTGACCACTTTGAATTTTGGCAGCATTTGGGAAAGGCGATTTTGGGAAGGTC 111
Db 195 GCCCACTTGGATCAGTTTGAACGATCAGACCCCTCGCACGGGCTCCTTCGGCGGGTG 254

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Search completed: May 28, 2004, 07:10:17

Job time : 25 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 26, 2004, 20:19:54 ; Search time 48 Seconds  
(without alignments)  
2365.024 Million cell updates/sec

Title: US-10-620-845-9  
Perfect score: 2151  
Sequence: 1 MGANTSRKPPVFEDNEDVNF.....VTNGQMDTGLSETQTQSKVS 407

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Sequences: 1149313 seqs, 278921704 residues

Total number of hits satisfying chosen parameters: 1149313

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubaa/US07\_PUBCOMB.pap:\*
- 2: /cgn2\_6/ptodata/1/pubaa/PCT\_NEW\_PUB.pap:\*
- 3: /cgn2\_6/ptodata/1/pubaa/US06\_NEW\_PUB.pap:\*
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- 6: /cgn2\_6/ptodata/1/pubaa/PCTUS\_PUBCOMB.pap:\*
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- 13: /cgn2\_6/ptodata/1/pubaa/US09E\_PUBCOMB.pap:\*
- 14: /cgn2\_6/ptodata/1/pubaa/US10A\_PUBCOMB.pap:\*
- 15: /cgn2\_6/ptodata/1/pubaa/US10B\_PUBCOMB.pap:\*
- 16: /cgn2\_6/ptodata/1/pubaa/US10C\_PUBCOMB.pap:\*
- 17: /cgn2\_6/ptodata/1/pubaa/US10D\_PUBCOMB.pap:\*
- 18: /cgn2\_6/ptodata/1/pubaa/US60\_NEW\_PUB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2151	100.0	407	9	US-09-841-683-9
2	2060	95.8	396	9	US-09-841-683-11
3	2060	95.8	396	12	US-10-362-892-20
4	2060	95.8	396	12	US-10-182-243-33
5	2060	95.8	396	15	US-10-288-798-20
6	2054	95.5	396	15	US-10-410-764-101
7	2047	95.2	396	9	US-09-801-876B-2
8	2047	95.2	396	12	US-10-667-442-2
9	2047	95.2	396	14	US-10-254-869-2
10	1827	84.9	358	15	US-10-108-260A-2674
11	1441	67.0	414	15	US-10-074-978A-158
12	1430.5	66.5	404	9	US-03-801-876B-4
13	1430.5	66.5	404	12	US-10-667-442-4
14	1430.5	66.5	404	14	US-10-254-869-4
15	1423.5	66.2	403	9	US-09-801-876B-5

16	1423.5	66.2	403	12	US-10-667-442-5	Sequence 5, Appli
17	1423.5	66.2	403	14	US-10-254-869-5	Sequence 5, Appli
18	1423.5	66.2	414	14	US-10-354-358-36	Sequence 36, Appli
19	1423.5	66.2	414	15	US-10-074-978A-157	Sequence 157, App
20	1333.5	62.0	488	15	US-10-074-978A-154	Sequence 154, App
21	1332.5	61.9	419	9	US-09-799-875-14	Sequence 14, Appli
22	1332.5	61.9	419	12	US-10-649-156-14	Sequence 14, Appli
23	1332.5	61.9	419	14	US-10-303-664A-6	Sequence 6, Appli
24	1331	61.8	485	12	US-10-415-011-12	Sequence 12, Appli
25	1328.5	61.8	384	9	US-09-801-876B-6	Sequence 6, Appli
26	1328.5	61.8	384	12	US-10-667-442-6	Sequence 6, Appli
27	1328.5	61.8	384	14	US-10-254-869-6	Sequence 6, Appli
28	1310.5	60.9	488	15	US-10-074-978A-18	Sequence 18, Appli
29	1294.5	60.2	399	10	US-09-819-607-4	Sequence 4, Appli
30	1294.5	60.2	399	12	US-10-633-631-4	Sequence 4, Appli
31	1272.5	59.2	375	12	US-10-168-582-12	Sequence 12, Appli
32	1186.5	55.2	364	12	US-10-206-915-572	Sequence 572, App
33	1186.5	55.2	364	12	US-10-199-670-572	Sequence 572, App
34	1186.5	55.2	364	12	US-10-201-858-572	Sequence 572, App
35	1186.5	55.2	364	12	US-10-205-890-572	Sequence 572, App
36	1186.5	55.2	364	12	US-10-208-024-572	Sequence 572, App
37	1186.5	55.2	364	12	US-10-201-853-572	Sequence 572, App
38	1186.5	55.2	364	12	US-10-174-581-572	Sequence 572, App
39	1186.5	55.2	364	12	US-10-176-483-572	Sequence 572, App
40	1186.5	55.2	364	12	US-10-176-749-572	Sequence 572, App
41	1186.5	55.2	364	12	US-10-176-914-572	Sequence 572, App
42	1186.5	55.2	364	12	US-10-176-915-572	Sequence 572, App
43	1186.5	55.2	364	12	US-10-176-484-572	Sequence 572, App
44	1186.5	55.2	364	12	US-10-180-550-572	Sequence 572, App
45	1186.5	55.2	364	12	US-10-183-014-572	Sequence 572, App

## ALIGNMENTS

RESULT 1  
US-09-841-683-9  
; Sequence 9, Application US/09841683  
; Patent No. US20020081600A1  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Yi  
; APPLICANT: Nepomichy, Boris  
; APPLICANT: Wang, Xiaoming  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Scoville, John  
; APPLICANT: Walke, D. Wade  
; TITLE OF INVENTION: No. US20020081600A1 Human Kinase Proteins and Polynucleotides Et  
; FILE REFERENCE: LEX-0167-USA  
; CURRENT APPLICATION NUMBER: US/09/841,683  
; CURRENT FILING DATE: 2001-04-24  
; PRIOR APPLICATION NUMBER: US 60/199,499  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: US 60/201,227  
; PRIOR FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 407  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-841-683-9

Query Match 100.0%; Score 2151; DB 9; Length 407;  
Best Local Similarity 100.0%; Pred. No. 1.2e-170;  
Matches 407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGANTSRKPPVFEDNEDVNFDPHFEILRAIGKSGFGKVCIVQKNDTKKQYAMKYNKQKV 60  
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QY 61 ERNEVRNVKELQIMOGLEHPFLVNLWYSPQDEDMFVVDLLGGDLRYHLQONVHFE 120  
Db 61 ERNEVRNVKELQIMOGLEHPFLVNLWYSPQDEDMFVVDLLGGDLRYHLQONVHFE 120

Qy 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180  
Db 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180  
Qy 181 AGTKPYMAPFMFSRRKAGYSFADWWSLGVATYELLGRPRPHIRSSSTSSKEIVHTFET 240  
Db 181 AGTKPYMAPFMFSRRKAGYSFADWWSLGVATYELLGRPRPHIRSSSTSSKEIVHTFET 240  
Qy 241 TVVTYPSAWSQEMVSLKLLLEPNPDORFQSDVQNPFPYNDINWDAVFOKRLIPGFI 300  
Db 241 TVVTYPSAWSQEMVSLKLLLEPNPDORFQSDVQNPFPYNDINWDAVFOKRLIPGFI 300  
Qy 301 NKGRINCDPTFELEMILESKPLHKKRKLAKKEDKMRKCDSSQTCLLQEHLDVQKEFI 360  
Db 301 NKGRINCDPTFELEMILESKPLHKKRKLAKKEDKMRKCDSSQTCLLQEHLDVQKEFI 360  
Qy 361 IFNREKVRNDRFNKQPNALBQTKDPQVNTGOMDTGLSETFQTSKVS 407  
Db 361 IFNREKVRNDRFNKQPNALBQTKDPQVNTGOMDTGLSETFQTSKVS 407  
RESULT 2  
US-9-841-683-11  
Sequence 11, Application US/09841683  
Publication No. US20020081600A1  
GENERAL INFORMATION:  
APPLICANT: Hu, Yi  
APPLICANT: Nepomniachy, Boris  
APPLICANT: Wang, Xiaoming  
APPLICANT: Donoho, Gregory  
APPLICANT: Scoville, John  
APPLICANT: Walke, D. Wade  
TITLE OF INVENTION: No. US20020081600A1el Human Kinase Proteins and Polynucleotides  
FILE REFERENCE: LEX-0167-USA  
CURRENT APPLICATION NUMBER: US/09/841,683  
PRIOR FILING DATE: 2001-04-24  
PRIOR APPLICATION NUMBER: US 60/199,499  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: US 60/201,227  
PRIOR FILING DATE: 2000-05-01  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: FAST-SEQ for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 396  
TYPE: PRT  
ORGANISM: homo sapiens  
US-9-841-683-11  
Query Match 95.8%; Score 2060; DB 9; Length 396;  
Best Local Similarity 99.2%; Pred. No. 4.5e-163;  
Matches 389; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKV 60  
Db 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKV 60  
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Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFE 120  
Qy 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180  
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Qy 181 AGTKPYMAPFMFSRRKAGYSFADWWSLGVATYELLGRPRPHIRSSSTSSKEIVHTFET 240  
Db 181 AGTKPYMAPFMFSRRKAGYSFADWWSLGVATYELLGRPRPHIRSSSTSSKEIVHTFET 240  
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Db 241 TVVTYPSAWSQEMVSLKLLLEPNPDORFQSDVQNPFPYNDINWDAVFOKRLIPGFI 300

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Db 301 NKGRINCDPTFELEMILESKPLHKKRKLAKKEDKMRKCDSSQTCLLQEHLDVQKEFI 360  
Qy 361 IFNREKVRNDRFNKQPNALBQTKDPQVNTGOMDTGLSETFQTSKVS 392  
Db 361 IFNREKVRNDRFNKQPNALBQTKDPQVNTGOMDTGLSETFQTSKVS 392  
RESULT 3  
US-10-362-892-20  
Sequence 20, Application US/10362892  
Publication No. US20040038881A1  
GENERAL INFORMATION:  
APPLICANT: INCYTE GENOMICS, INC.; BANDMAN, Olga  
APPLICANT: NGUYEN, Daniel B.; WALLIA, Narinder K.  
APPLICANT: HAPALIA, April J.A.; YAO, Monique G.  
APPLICANT: GANDHI, Ameena R.; GURURAJAN, Rajagopal  
APPLICANT: DING, Li; PATTERSON, Chandra S.  
APPLICANT: YUE, Henry; BAUGHN, Mariah R.  
APPLICANT: TRIBOULEY, Catherine M.; THORNTON, Michael B.  
APPLICANT: ELLIOTT, Vicki S.; LU, Yan  
APPLICANT: ISON, Craig H.; AU-YOUNG, Janice K.  
APPLICANT: TANG, Y. Tom; AZIMZAI, Yalda  
APPLICANT: BURRILL, John D.; MARCUS, Gregory A.  
APPLICANT: ZINGLER, Kurt A.; LU, Dyung Aina M.  
APPLICANT: LAL, Preeti G.; RAMKUMAR, Javalaxmi  
APPLICANT: WARREN, Bridget A.; KEARNEY, Liam  
APPLICANT: POLICKY, Jennifer L.; THANGAVELU, Kavitha  
APPLICANT: BURFORD, Neil  
TITLE OF INVENTION: HUMAN KINASES  
FILE REFERENCE: PF-0209 USN  
CURRENT APPLICATION NUMBER: US/10/362,892  
CURRENT FILING DATE: 2003-02-25  
PRIOR APPLICATION NUMBER: PCT/US01/27219  
PRIOR FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: US 60/229,873  
PRIOR FILING DATE: 2000-08-31  
PRIOR APPLICATION NUMBER: US 60/231,357  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: US 60/232,654  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: US 60/234,902  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: US 60/236,499  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: US 60/238,389  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: US 60/240,542  
PRIOR FILING DATE: 2000-10-13  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PERL Program  
SEQ ID NO 20  
LENGTH: 396  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. US20040038881A1 7946584CD1  
US-10-362-892-20  
Query Match 95.8%; Score 2060; DB 12; Length 396;  
Best Local Similarity 99.2%; Pred. No. 4.5e-163;  
Matches 389; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKV 60  
Db 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKV 60  
Qy 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFE 120  
Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFE 120



QY 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNLLDEHGHVHTDFTNIAAMLPRETOITTM 180  
Db 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNLLDEHGHVHTDFTNIAAMLPRETOITTM 180  
QY 181 AGTKPYMAPEMPSSRKAGYSFAVDWWSLGVTAELLRGRPPYHRSSTSSKEIVHTFET 240  
Db 181 AGTKPYMAPEMPSSRKAGYSFAVDWWSLGVTAELLRGRPPYHRSSTSSKEIVHTFET 240  
QY 241 TVVTYPSAWSQEMWSLLKLEPNPDPQFSQSDVQNFYMNNDINWDAVFOKRLIPGP 300  
Db 241 TVVTYPSAWSQEMWSLLKLEPNPDPQFSQSDVQNFYMNNDINWDAVFOKRLIPGP 300  
QY 301 NGRNLNCDPTFELEEMILESPLHKKKRLAKKEKMDKCDSSQTCLOEHLDSVQKEFI 360  
Db 301 NGRNLNCDPTFELEEMILESPLHKKKRLAKKEKMDKCDSSQTCLOEHLDSVQKEFI 360  
QY 361 IFNREKVNDRFNKROPNLALQTKDPQVINGQ 392  
Db 361 IFNREKVNDRFNKROPNLALQTKDPQVINGQ 392  
RESULT 4  
US-10-182-243-33  
; Sequence 33, Application US/10182243  
; Publication No. US20040048310A1  
; GENERAL INFORMATION:  
; APPLICANT: FLOWMAN, GREGORY D.  
; APPLICANT: WHYTE, DAVID  
; APPLICANT: MANNING, GERARD  
; APPLICANT: SUDARSANAM, SUCHA  
; APPLICANT: MARTINEZ, RICARDO  
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE  
; TITLE OF INVENTION: ENZYMES  
; FILE REFERENCE: 038602/1366  
; CURRENT APPLICATION NUMBER: US/10/182,243  
; PRIOR FILING DATE: 2003-07-07  
; PRIOR APPLICATION NUMBER: PCT/US01/02337  
; PRIOR FILING DATE: 2001-01-25  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 33  
; LENGTH: 396  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: Incyte ID No. US20030207299A1 7946584CD1  
US-10-182-243-33  
Query Match 95.8%; Score 2060; DB 12; Length 396;  
Best Local Similarity 99.2%; Pred. No. 4.5e-163;  
Matches 389; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKCV 60  
Db 1 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKCV 60  
QY 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFKE 120  
Db 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFKE 120  
QY 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNLLDEHGHVHTDFTNIAAMLPRETOITTM 180  
Db 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNLLDEHGHVHTDFTNIAAMLPRETOITTM 180  
QY 181 AGTKPYMAPEMPSSRKAGYSFAVDWWSLGVTAELLRGRPPYHRSSTSSKEIVHTFET 240  
Db 181 AGTKPYMAPEMPSSRKAGYSFAVDWWSLGVTAELLRGRPPYHRSSTSSKEIVHTFET 240  
QY 241 TVVTYPSAWSQEMWSLLKLEPNPDPQFSQSDVQNFYMNNDINWDAVFOKRLIPGP 300  
Db 241 TVVTYPSAWSQEMWSLLKLEPNPDPQFSQSDVQNFYMNNDINWDAVFOKRLIPGP 300  
QY 301 NGRNLNCDPTFELEEMILESPLHKKKRLAKKEKMDKCDSSQTCLOEHLDSVQKEFI 360  
Db 301 NGRNLNCDPTFELEEMILESPLHKKKRLAKKEKMDKCDSSQTCLOEHLDSVQKEFI 360

QY 361 IFNREKVNDRFNKROPNLALQTKDPQVINGQ 392  
Db 361 IFNREKVNDRFNKROPNLALQTKDPQVINGQ 392  
RESULT 5  
US-10-288-798-20  
; Sequence 20, Application US/10288798  
; Publication No. US20030207299A1  
; GENERAL INFORMATION:  
; APPLICANT: BANDMAN, Olga; NGUYEN, Danniell B.;  
; APPLICANT: WALIA, Narinder K.; HAFALIA, April J.A.;  
; APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;  
; APPLICANT: GURURAJAN, Rajagopal; DING, Li;  
; APPLICANT: PATTERSON, Chandra; YUE, Henry;  
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;  
; APPLICANT: THORNTON, Michael; ELLIOTT, Vicki S.;  
; APPLICANT: LU, Yan; ISON, Craig H.;  
; APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;  
; APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;  
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;  
; APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.;  
; APPLICANT: RAMKOMAR, Jayalaxmi; WARREN, Bridget A.;  
; APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;  
; APPLICANT: THANGAVELU, Kavitha; BURFORD, Neil  
; TITLE OF INVENTION: HUMAN KINASES  
; FILE REFERENCE: PI-0209 USA  
; CURRENT APPLICATION NUMBER: US/10/288,798  
; CURRENT FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: PCT/US01/27219  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/240,542  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: US 60/238,389  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: US 60/236,499  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: US 60/234,902  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: US 60/232,654  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: US 60/231,357  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: US 60/229,873  
; PRIOR FILING DATE: 2000-08-31  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PERL Program  
; SEQ ID NO 20  
; LENGTH: 396  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030207299A1 7946584CD1  
US-10-288-798-20  
Query Match 95.8%; Score 2060; DB 15; Length 396;  
Best Local Similarity 99.2%; Pred. No. 4.5e-163;  
Matches 389; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKCV 60  
Db 1 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKCV 60  
QY 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFKE 120  
Db 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFKE 120  
QY 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNLLDEHGHVHTDFTNIAAMLPRETOITTM 180  
Db 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNLLDEHGHVHTDFTNIAAMLPRETOITTM 180

QY 181 AGTKPYMAPEMFSSRKAGYSAVDWWSLGVYAYELLGRRPYHRSSTSSKEIVHTPET 240  
 Db 181 AGTKPYMAPEMFSSRKAGYSAVDWWSLGVYAYELLGRRPYHRSSTSSKEIVHTPET 240  
 QY 241 TVVTYPSAWSQEMVSLKLLKLEPNPDRFQSDVQNFYPMNDINWDVAVFQKRLIPGIP 300  
 Db 241 TVVTYPSAWSQEMVSLKLLKLEPNPDRFQSDVQNFYPMNDINWDVAVFQKRLIPGIP 300  
 QY 301 NGRINCDPTFELEEMILESPLHKKKRLAKKEDMRKCDSSQTCLLQEHLDVQKEFI 360  
 Db 301 NGRINCDPTFELEEMILESPLHKKKRLAKKEDMRKCDSSQTCLLQEHLDVQKEFI 360  
 QY 361 IFNREKVNDRDNKOPNLALEQTKDPQVINGQ 392  
 Db 361 IFNREKVNDRDNKOPNLALEQTKDPQGEDGQ 392

RESULT 6  
 US-10-410-764-101  
 ; Sequence 101, Application US/10410764  
 ; Patent No. US20040005664A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Millennium Pharmaceuticals, Inc.  
 ; APPLICANT: Meyers, Rachel E.  
 ; APPLICANT: MacBeth, Kyle J.  
 ; APPLICANT: Curtis, Rory A.J.  
 ; APPLICANT: Rudolph-Owen, Laura A.  
 ; APPLICANT: Weich, Nadine S.  
 ; APPLICANT: Tsai, Fong-Ying  
 ; APPLICANT: Kapeller-Liebermann, Rosana  
 ; APPLICANT: Carroll, Joseph M.  
 ; TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50266,  
 ; TITLE OF INVENTION: 58764, 62113, 32144, 32235, 23565, 13305, 14911, 86216,  
 ; TITLE OF INVENTION: 25206 AND 8843 MOLECULES AND USES THEREFOR  
 ; FILE REFERENCE: MPT03-0520NMIM  
 ; CURRENT APPLICATION NUMBER: US/10/410,764  
 ; CURRENT FILING DATE: 2003-04-10  
 ; PRIOR APPLICATION NUMBER: US 09/924,358  
 ; PRIOR FILING DATE: 2001-08-06  
 ; PRIOR APPLICATION NUMBER: US 60/229,300  
 ; PRIOR FILING DATE: 2000-09-01  
 ; PRIOR APPLICATION NUMBER: US 10/350,553  
 ; PRIOR FILING DATE: 2003-01-24  
 ; PRIOR APPLICATION NUMBER: US 60/351,572  
 ; PRIOR FILING DATE: 2002-01-24  
 ; PRIOR APPLICATION NUMBER: US 09/966,614  
 ; PRIOR FILING DATE: 2001-09-27  
 ; PRIOR APPLICATION NUMBER: US 60/238,054  
 ; PRIOR FILING DATE: 2000-10-05  
 ; PRIOR APPLICATION NUMBER: US 10/281,094  
 ; PRIOR FILING DATE: 2002-10-25  
 ; PRIOR APPLICATION NUMBER: US 60/347,815  
 ; PRIOR FILING DATE: 2001-10-29  
 ; PRIOR APPLICATION NUMBER: US 10/076,535  
 ; PRIOR FILING DATE: 2002-02-15  
 ; PRIOR APPLICATION NUMBER: US 60/269,440  
 ; PRIOR FILING DATE: 2001-02-16  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 136  
 ; SOFTWARE: Fast-Seq for Windows Version 4.0  
 ; SEQ ID NO 101  
 ; LENGTH: 396  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-410-764-101

Query Match 95.5%; Score 2054; DB 15; Length 396;  
 Best Local Similarity 99.0%; Pred. No. 1.4e-162;  
 Matches 388; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKKQYAMKYNKQKCV 60

Db 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKKQYAMKYNKQKCV 60  
 QY 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120  
 Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120  
 QY 121 ETVKLFICELVMDLYLQNRQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETIQITTM 180  
 Db 121 ETVKLFICELVMDLYLQNRQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETIQITTM 180  
 QY 181 AGTKPYMAPEMFSSRKAGYSAVDWWSLGVYAYELLGRRPYHRSSTSSKEIVHTPET 240  
 Db 181 AGTKPYMAPEMFSSRKAGYSAVDWWSLGVYAYELLGRRPYHRSSTSSKEIVHTPET 240  
 QY 241 TVVTYPSAWSQEMVSLKLLKLEPNPDRFQSDVQNFYPMNDINWDVAVFQKRLIPGIP 300  
 Db 241 TVVTYPSAWSQEMVSLKLLKLEPNPDRFQSDVQNFYPMNDINWDVAVFQKRLIPGIP 300  
 QY 301 NGRINCDPTFELEEMILESPLHKKKRLAKKEDMRKCDSSQTCLLQEHLDVQKEFI 360  
 Db 301 NGRINCDPTFELEEMILESPLHKKKRLAKKEDMRKCDSSQTCLLQEHLDVQKEFI 360  
 QY 351 IFNREKVNDRDNKOPNLALEQTKDPQVINGQ 392  
 Db 351 IFNREKVNDRDNKOPNLALEQTKDPQGEDGQ 392

RESULT 7  
 US-09-801-876B-2  
 ; Sequence 2, Application US/09801876B  
 ; Patent No. US20020127683A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: YE, Jane et al  
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
 ; TITLE OF INVENTION: THEREOF  
 ; FILE REFERENCE: CL001160  
 ; CURRENT APPLICATION NUMBER: US/09/801,876B  
 ; CURRENT FILING DATE: 2001-03-09  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: Fast-Seq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 396  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 ; US-09-801-876B-2

Query Match 95.2%; Score 2047; DB 9; Length 396;  
 Best Local Similarity 96.7%; Pred. No. 5.4e-162;  
 Matches 587; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKKQYAMKYNKQKCV 60  
 Db 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKKQYAMKYNKQKCV 60  
 QY 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120  
 Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120  
 QY 121 ETVKLFICELVMDLYLQNRQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETIQITTM 180  
 Db 121 ETVKLFICELVMDLYLQNRQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETIQITTM 180  
 QY 181 AGTKPYMAPEMFSSRKAGYSAVDWWSLGVYAYELLGRRPYHRSSTSSKEIVHTPET 240  
 Db 181 AGTKPYMAPEMFSSRKAGYSAVDWWSLGVYAYELLGRRPYHRSSTSSKEIVHTPET 240  
 QY 241 TVVTYPSAWSQEMVSLKLLKLEPNPDRFQSDVQNFYPMNDINWDVAVFQKRLIPGIP 300  
 Db 241 TVVTYPSAWSQEMVSLKLLKLEPNPDRFQSDVQNFYPMNDINWDVAVFQKRLIPGIP 300  
 QY 301 NGRINCDPTFELEEMILESPLHKKKRLAKKEDMRKCDSSQTCLLQEHLDVQKEFI 360



QY 181 AGTKPYMAPEMFSSRKAGYGFVNDWWSLGYTAVELLGRPPYHRSSTSSKEIVHTPET 240  
 DB 181 AGTKPYMAPEMFSSRKAGYGFVNDWWSLGYTAVELLGRPPYHRSSTSSKEIVHTPET 240  
 QY 241 TWTVPYSAWSQEMVSLKLLLEPPDPQRFSDQVQNFPPYNDINWDVAFQKRLIPGIP 300  
 DB 241 TWTVPYSAWSQEMVSLKLLLEPPDPQRFSDQVQNFPPYNDINWDVAFQKRLIPGIP 300  
 QY 301 NKGRINCDDPTFELEEMILESKPLHKKKRLAKKEMKCDSSQ 344  
 DB 301 NKGRINCDDPTFELEEMILESKPLHKKKRLAKKEMKCDSSQ 344

RESULT 11

US-10-074-978A-158  
 Sequence 158, Application US/10074978A  
 Publication No. US20040010119A1

GENERAL INFORMATION:

APPLICANT: Leite, Mario  
 APPLICANT: Spytek, Kimberly A  
 APPLICANT: Guo, Xiaojia (Sasha)  
 APPLICANT: Fernandes, Elma  
 APPLICANT: Li, Li  
 APPLICANT: Kekuda, Ramesh  
 APPLICANT: Liu, Xiahong  
 APPLICANT: Casman, Stacie  
 APPLICANT: Boldog, Ferenc  
 APPLICANT: Patturajan, Meera  
 APPLICANT: Blalock, Angela  
 APPLICANT: Ballinger, Robert  
 APPLICANT: Vernet, Corine  
 APPLICANT: Tchernev, Velizar T  
 APPLICANT: Malyankar, Uriel M  
 APPLICANT: Gusev, Vladimir  
 APPLICANT: Rastelli, Luca  
 APPLICANT: Mezes, Peter S  
 APPLICANT: Ellerman, Karen  
 APPLICANT: Hayes, Melvin P  
 APPLICANT: Herriman, John  
 APPLICANT: Pena, Carol E A  
 APPLICANT: Shimkets, Richard A  
 APPLICANT: Taupier Jr, Raymond J  
 APPLICANT: Moore, No. US20040010119A11le  
 APPLICANT: Shenoy, Suresh  
 APPLICANT: Edinger, Shlomit  
 APPLICANT: Gunther, Erik  
 APPLICANT: Stone, Dave  
 APPLICANT: Millet, Isabelle  
 APPLICANT: Payman, John  
 APPLICANT: Smithson, Glennda

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

FILE REFERENCE: 21402-269

CURRENT APPLICATION NUMBER: US/10/074.978A

PRIOR FILING DATE: 2003-01-07  
 PRIOR APPLICATION NUMBER: 60/268,221  
 PRIOR FILING DATE: 2001-02-12  
 PRIOR APPLICATION NUMBER: 60/335,109  
 PRIOR FILING DATE: 2001-10-31  
 PRIOR APPLICATION NUMBER: 60/312,284  
 PRIOR FILING DATE: 2001-08-14  
 PRIOR APPLICATION NUMBER: 60/268,496  
 PRIOR FILING DATE: 2001-02-13  
 PRIOR APPLICATION NUMBER: 60/276,703  
 PRIOR FILING DATE: 2001-03-16  
 PRIOR APPLICATION NUMBER: 60/330,293  
 PRIOR FILING DATE: 2001-10-18  
 PRIOR APPLICATION NUMBER: 60/322,127  
 PRIOR FILING DATE: 2001-11-21  
 PRIOR APPLICATION NUMBER: 60/280,899  
 PRIOR FILING DATE: 2001-04-02  
 PRIOR APPLICATION NUMBER: 60/310,797  
 PRIOR FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: 60/268,646

PRIOR FILING DATE: 2001-02-14

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 547

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 158

LENGTH: 414

TYPE: PRT

ORGANISM: Mus musculus

US-10-074-978A-158

Query Match 67.0%; Score 1441; DB 15; Length 414;

Best Local Similarity 68.3%; Pred. No. 1.1e-111;

Matches 280; Conservative 43; Mismatches 71; Indels 16; Gaps 4;

QY 1 MGANTSRKPPVFDENEVDNFDHFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60  
 DB 1 MGNHSHKPPVFDENEVDNFDHFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60  
 QY 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFE 120  
 DB 61 ERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFE 120  
 QY 121 ETVKLFICELVMDLYLQVORIIHRDKPDNILLDEHGHVHTDFTNIAMLPRETOITTM 180  
 DB 121 GTVKLYICELALALEYLQRYHIIHRDKPDNILLDEHGHVHTDFTNIAMLPRETOITTM 180  
 QY 181 AGTKPYMAPEMFS--SRKAGYGFVNDWWSLGYTAVELLGRPPYHRSSTSSKEIVHTF 238  
 DB 181 AGTKPYMAPEVFQVYDGGFGYFVDWWSLGYTAVELLGRPPYHRSATPDEILNMF 240  
 QY 239 ETTVTVPYSAWSQEMVSLKLLLEPPDPQRFSDQVQNFPPYNDINWDVAFQKRLIPGF 298  
 DB 241 KVERVHYSTWCBSGMVSLKLLTKDPESSLRDIQSMYTLADNMWDVAFKALMPGF 300  
 QY 299 IPNKGRLNCDDPTFELEEMILESKPLHKKKRLAK-KEKDMKCDSSOTCLLOHLDVQK 357  
 DB 301 VPNKGRLNCDDPTFELEEMILESKPLHKKKRLAKHRSRSTKDCSPINGHLOQCLETVRK 360  
 QY 358 EFTIFNREKVNRFNKRQPNLALEQTKDPQVT--NGQMDTGLSETFQTSK 405  
 DB 361 EFTIFNREKLRR-----QQGHGQLSLDGRIGSQTSSKLDGR 399

RESULT 12

US-09-801-876B-4

Sequence 4, Application US/09801876B

Patent No. US20020127683A1

GENERAL INFORMATION:

APPLICANT: YE, Jane et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

FILE REFERENCE: CL001160

CURRENT APPLICATION NUMBER: US/09/801,876B

CURRENT FILING DATE: 2001-03-09

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4

LENGTH: 404

TYPE: PRT

ORGANISM: Mus Musculus

US-09-801-876B-4

Query Match 66.5%; Score 1430.5; DB 9; Length 404;

Best Local Similarity 68.1%; Pred. No. 1.1e-110;

Matches 280; Conservative 43; Mismatches 71; Indels 17; Gaps 5;

QY 1 MGANTSRKPPVFDENEVDNFDHFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60  
 DB 1 MGNHSHKPPVFDENEVDNFDHFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60  
 QY 61 -ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFE 119

Db 61 QERDEVNRVRELQIMQGLEHFFELRAIGKSGFKVCIVQKNDTKKMYAMKMKQKCV 120  
QY 120 BETVKLFICELVMDYLNQRIIHRDKMKNPNDLDEGHVHITDFNTAAMLPRETQIT 179  
Db 121 EGTVKLYICELALALEYLRVHIHRDKMKNPNDLDEGHVHITDFNTAAMLPRETQIT 180  
QY 180 MAGTKPYMAPEMFS--SRKGAGYFAVDWMSLGVTAELLGRPPYHRSSTSSKEIVHT 237  
Db 181 MAGTKPYMAPEMFS--SRKGAGYFAVDWMSLGVTAELLGRPPYHRSSTSSKEIVHT 240  
QY 238 FETTVVTPSAWSQEMVSLKLLKLEPNDFQSFQSDVQNPYMDINWDAVFOKRLIPG 297  
Db 241 FKVERVHSSVTCWEGWVSLKLLKLEPNDFQSFQSDVQNPYMDINWDAVFOKRLIPG 300  
QY 298 FIPNKGRLNCDPTFELEEMILESPLHKKKRLAK-KEKDMKCDSSOTCLLQHLDSVQ 356  
Db 301 FVPNKGRLNCDPTFELEEMILESPLHKKKRLAK-KEKDMKCDSSOTCLLQHLDSVQ 360  
QY 357 KEFIIFNREKVRNDRFNKQPNALAEQTKDPQVT--NGQMDTGLSETFTQSK 405  
Db 361 KEFIIFNREKVRNDRFNKQPNALAEQTKDPQVT--NGQMDTGLSETFTQSK 400  
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US-10-667-442-4  
; Sequence 4, Application US/10667442  
; Publication No. US20040043466A1  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001160DIV II  
; CURRENT FILING DATE: 2003-09-23  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 404  
; TYPE: PRT  
; ORGANISM: Mus Musculus  
US-10-667-442-4  
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Best Local Similarity 68.1%; Pred. No. 1.1e-110;  
Matches 280; Conservative 43; Mismatches 71; Indels 17; Gaps 5;  
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121 EGTVKLYICELALALEYLRVHIHRDKMKNPNDLDEGHVHITDFNTAAMLPRETQIT 180  
180 MAGTKPYMAPEMFS--SRKGAGYFAVDWMSLGVTAELLGRPPYHRSSTSSKEIVHT 237  
181 MAGTKPYMAPEMFS--SRKGAGYFAVDWMSLGVTAELLGRPPYHRSSTSSKEIVHT 240  
238 FETTVVTPSAWSQEMVSLKLLKLEPNDFQSFQSDVQNPYMDINWDAVFOKRLIPG 297  
241 FKVERVHSSVTCWEGWVSLKLLKLEPNDFQSFQSDVQNPYMDINWDAVFOKRLIPG 300  
298 FIPNKGRLNCDPTFELEEMILESPLHKKKRLAK-KEKDMKCDSSOTCLLQHLDSVQ 356  
301 FVPNKGRLNCDPTFELEEMILESPLHKKKRLAK-KEKDMKCDSSOTCLLQHLDSVQ 360  
357 KEFIIFNREKVRNDRFNKQPNALAEQTKDPQVT--NGQMDTGLSETFTQSK 405

Db 361 KEFIIFNREKVRNDRFNKQPNALAEQTKDPQVT--NGQMDTGLSETFTQSK 400  
RESULT 14  
US-10-254-869-4  
; Sequence 4, Application US/10254869  
; Publication No. US20030027307A1  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001160DIV  
; CURRENT FILING DATE: 2002-09-26  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 404  
; TYPE: PRT  
; ORGANISM: Mus Musculus  
US-10-254-869-4  
Query Match 66.5%; Score 1430.5; DB 14; Length 404;  
Best Local Similarity 68.1%; Pred. No. 1.1e-110;  
Matches 280; Conservative 43; Mismatches 71; Indels 17; Gaps 5;  
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61 -ERNEVRNVFRELQIMQGLEHFFELRAIGKSGFKVCIVQKNDTKKMYAMKMKQKCV 119  
61 QERDEVNRVRELQIMQGLEHFFELRAIGKSGFKVCIVQKNDTKKMYAMKMKQKCV 120  
120 BETVKLFICELVMDYLNQRIIHRDKMKNPNDLDEGHVHITDFNTAAMLPRETQIT 179  
121 EGTVKLYICELALALEYLRVHIHRDKMKNPNDLDEGHVHITDFNTAAMLPRETQIT 180  
180 MAGTKPYMAPEMFS--SRKGAGYFAVDWMSLGVTAELLGRPPYHRSSTSSKEIVHT 237  
181 MAGTKPYMAPEMFS--SRKGAGYFAVDWMSLGVTAELLGRPPYHRSSTSSKEIVHT 240  
238 FETTVVTPSAWSQEMVSLKLLKLEPNDFQSFQSDVQNPYMDINWDAVFOKRLIPG 297  
241 FKVERVHSSVTCWEGWVSLKLLKLEPNDFQSFQSDVQNPYMDINWDAVFOKRLIPG 300  
298 FIPNKGRLNCDPTFELEEMILESPLHKKKRLAK-KEKDMKCDSSOTCLLQHLDSVQ 356  
301 FVPNKGRLNCDPTFELEEMILESPLHKKKRLAK-KEKDMKCDSSOTCLLQHLDSVQ 360  
357 KEFIIFNREKVRNDRFNKQPNALAEQTKDPQVT--NGQMDTGLSETFTQSK 405  
Db 361 KEFIIFNREKVRNDRFNKQPNALAEQTKDPQVT--NGQMDTGLSETFTQSK 400  
RESULT 15  
US-09-801-876B-5  
; Sequence 5, Application US/09801876B  
; Patent No. US20020127683A1  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001160  
; CURRENT FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 403

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Copied from 10260845 on 08/11/2005

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OM protein - protein search, using sw model

Run on: May 26, 2004, 20:17:13 ; Search time 23 Seconds  
(without alignments)  
913.555 Million cell updates/sec

Title: US-10-620-845-9

Perfect score: 2151

Sequence: 1 MGANTSRRKPPVDENEDVNF.....VTNGQMDTGLSETFOTSKVS 407

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Seached: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/prodata/2/iaa/5A COMB.pap:\*

2: /cgn2\_6/prodata/2/iaa/5B COMB.pap:\*

3: /cgn2\_6/prodata/2/iaa/6A COMB.pap:\*

4: /cgn2\_6/prodata/2/iaa/6B COMB.pap:\*

5: /cgn2\_6/prodata/2/iaa/6C COMB.pap:\*

6: /cgn2\_6/prodata/2/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	ID	Description
1	2151	100.0	407	US-09-841-683-9	Sequence 9, Appli
2	2060	95.8	396	US-09-841-683-11	Sequence 11, Appli
3	2047	95.2	396	US-09-801-8768-2	Sequence 2, Appli
4	2047	95.2	396	US-10-254-869-2	Sequence 2, Appli
5	1430.5	66.5	404	US-09-801-8768-4	Sequence 4, Appli
6	1430.5	66.5	404	US-10-254-869-4	Sequence 4, Appli
7	1423.5	66.2	403	US-09-801-8768-5	Sequence 5, Appli
8	1423.5	66.2	403	US-10-254-869-5	Sequence 5, Appli
9	1328.5	61.9	419	US-09-799-875-14	Sequence 14, Appli
10	1328.5	61.8	384	US-09-801-8768-6	Sequence 6, Appli
11	1328.5	61.8	384	US-10-254-869-6	Sequence 6, Appli
12	1294.5	60.2	399	US-09-819-607-4	Sequence 4, Appli
13	1174	54.6	236	US-09-841-683-7	Sequence 7, Appli
14	1171	54.4	225	US-09-841-683-5	Sequence 5, Appli
15	1142	53.1	369	US-09-819-607-2	Sequence 2, Appli
16	1127.5	52.4	368	US-09-819-607-5	Sequence 5, Appli
17	995.5	46.3	316	US-09-801-8768-7	Sequence 7, Appli
18	995.5	46.3	316	US-10-254-869-7	Sequence 7, Appli
19	852.5	39.6	347	US-09-801-8768-8	Sequence 8, Appli
20	852.5	39.6	347	US-10-254-869-8	Sequence 8, Appli
21	509.5	23.7	336	US-09-394-455-2	Sequence 2, Appli
22	509.5	23.7	343	US-09-394-455-15	Sequence 15, Appli
23	509.5	23.7	343	US-09-394-455-34	Sequence 34, Appli
24	509.5	23.7	351	US-09-394-455-4	Sequence 4, Appli
25	508.5	23.6	587	US-08-313-274-2	Sequence 2, Appli
26	503.5	23.4	343	US-09-394-455-38	Sequence 38, Appli
27	503.5	23.4	350	US-09-457-0408-37	Sequence 37, Appli

28	503.5	23.4	351	4	US-09-457-0408-6	Sequence 6, Appli
29	503.5	23.4	595	4	US-09-417-197-69	Sequence 69, Appli
30	498.5	23.2	689	1	US-08-221-817-18	Sequence 18, Appli
31	498.5	23.2	689	1	US-08-454-439-18	Sequence 18, Appli
32	498.5	23.2	689	5	PCT-US94-10487-18	Sequence 18, Appli
33	485.5	22.6	699	1	US-08-221-817-20	Sequence 20, Appli
34	485.5	22.6	699	1	US-08-454-439-20	Sequence 20, Appli
35	485.5	22.6	699	5	PCT-US94-10487-20	Sequence 20, Appli
36	485	22.5	260	2	US-07-857-224B-8	Sequence 8, Appli
37	484	22.5	260	2	US-07-857-224B-7	Sequence 7, Appli
38	481	22.4	480	3	US-09-091-058-2	Sequence 2, Appli
39	481	22.4	726	4	US-09-417-197-71	Sequence 71, Appli
40	481	22.4	727	4	US-09-417-197-139	Sequence 139, App
41	476.5	22.2	482	4	US-09-430-564-2	Sequence 2, Appli
42	476.5	22.2	495	4	US-09-430-564-3	Sequence 3, Appli
43	475.5	22.1	688	1	US-08-221-817-19	Sequence 19, Appli
44	475.5	22.1	688	1	US-08-454-439-19	Sequence 19, Appli
45	475.5	22.1	688	5	PCT-US94-10487-19	Sequence 19, Appli

ALIGNMENTS

RESULT 1  
US-09-841-683-9  
; Sequence 9, Application US/09841683  
; Patent No. 6617147  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Yi  
; APPLICANT: Nepomichy, Boris  
; APPLICANT: Wang, Xiaoming  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Scoville, John  
; APPLICANT: Walke, D, Wade  
; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding t  
; FILE REFERENCE: LEX-0167-USA  
; CURRENT APPLICATION NUMBER: US/09/841,683  
; PRIOR FILING DATE: 2001-04-24  
; PRIOR APPLICATION NUMBER: US 60/199,499  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: US 60/201,227  
; PRIOR FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-841-683-9

Query Match	100.0%	Score 2151;	DB 4;	Length 407;
Best Local Similarity	100.0%	Pred. No. 1.2e-197;	Mismatches 0;	Indels 0; Gaps 0;
Matches 407;	Conservative 0;			
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Db	1	MGANTSRRKPPVDENEDVNF	FDHFEILRAIGKSGFKGVCIVQKNDTKKMYAMKYNKQCV	60
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Db	6	ERNEVRNVFKELQIQMOGLEHPLVNLWTSFQDEDMFVVDLLGGDLRYHLQONVHFE	120	
QY	12	ETVKLFICELWALDYLNQRIIHRDMKPDNILLDEHGHVHTDENIAAMLPRETCITTM	180	
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QY	18	AGTKPYMAPEMFSSRRKAGYSFAVDWNSLGYTAYELLGRPRPHIRSSSTSSKEIVHTFET	240	
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Db	24	TVVTYPSAWSQEMVSLKKLLEPNPDQRFQSLQVQNPYPYNDINWDVAFQKRLIPGP	300	



QY 301 NKGRINCDPTTELEEMILESPLHKKKRLAKKEMKDKCDSSQTCLLQEHLDVSQKEFI 360  
 Db 301 NKGRINCDPTTELEEMILESPLHKKKRLAKKEMKDKCDSSQTCLLQEHLDVSQKEFI 360  
 QY 361 IFNREKVNDRDNKRNPNALALQTKDPQVTNGQMDTGLSETTQTSKVS 407  
 Db 361 IFNREKVNDRDNKRNPNALALQTKDPQVTNGQMDTGLSETTQTSKVS 407

RESULT 2  
 US-09-841-683-11  
 ; Sequence 11, Application US/09841683  
 ; Patent No. 6617147  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hu, Yi  
 ; APPLICANT: Nepomnichy, Boris  
 ; APPLICANT: Wang, Xiaoming  
 ; APPLICANT: Donoho, Gregory  
 ; APPLICANT: Scoville, John  
 ; APPLICANT: Walke, D. Wade  
 ; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding  
 ; FILE REFERENCE: LEX-0167-USA  
 ; CURRENT APPLICATION NUMBER: US/09/841,683  
 ; PRIOR FILING DATE: 2001-04-24  
 ; PRIOR APPLICATION NUMBER: US 60/199,499  
 ; PRIOR FILING DATE: 2000-04-25  
 ; PRIOR APPLICATION NUMBER: US 60/201,227  
 ; PRIOR FILING DATE: 2000-05-01  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 11  
 ; LENGTH: 396  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 ; US-09-841-683-11

Query Match 95.8%; Score 2060; DB 4; Length 396;  
 Best Local Similarity 99.2%; Pred. No. 5.9e-189;  
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 Db 61 ERNEVRNVFKELQIMQGLEHPLFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120  
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 Db 121 ETVKLFICELVMDLYLQONRIHRDMKPNLILDEHGHVHTDNTAAMLPRETOITTM 180  
 QY 181 AGTPEYMAPEMFSSRKAGYGFVADWMSLGVTVAYELLGRPPYHIRSTSSKEIVHTPET 240  
 Db 181 AGTPEYMAPEMFSSRKAGYGFVADWMSLGVTVAYELLGRPPYHIRSTSSKEIVHTPET 240  
 QY 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFQSDVQNPFPYNDINWDVAVFQKRLIPGIP 300  
 Db 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFQSDVQNPFPYNDINWDVAVFQKRLIPGIP 300  
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 Db 301 NKGRINCDPTTELEEMILESPLHKKKRLAKKEMKDKCDSSQTCLLQEHLDVSQKEFI 360  
 QY 361 IFNREKVNDRDNKRNPNALALQTKDPQVTNGQ 392  
 Db 361 IFNREKVNDRDNKRNPNALALQTKDPQVTNGQ 392

RESULT 3  
 US-09-801-876B-2  
 ; Sequence 2, Application US/09801876B

Patent No. 6492155  
 ; GENERAL INFORMATION:  
 ; APPLICANT: YE, Jane et al  
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
 ; TITLE OF INVENTION: THEREOF  
 ; FILE REFERENCE: CL001160  
 ; CURRENT APPLICATION NUMBER: US/09/801,876B  
 ; CURRENT FILING DATE: 2001-03-09  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 396  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 ; US-09-801-876B-2

Query Match 95.2%; Score 2047; DB 4; Length 396;  
 Best Local Similarity 98.7%; Pred. No. 1e-187;  
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 Db 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVOKNDTKMYAMKYNKQCV 60  
 QY 61 ERNEVRNVFKELQIMQGLEHPLFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120  
 Db 61 ERNEVRNVFKELQIMQGLEHPLFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120  
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 Db 121 ETVKLFICELVMDLYLQONRIHRDMKPNLILDEHGHVHTDNTAAMLPRETOITTM 180  
 QY 181 AGTPEYMAPEMFSSRKAGYGFVADWMSLGVTVAYELLGRPPYHIRSTSSKEIVHTPET 240  
 Db 181 AGTPEYMAPEMFSSRKAGYGFVADWMSLGVTVAYELLGRPPYHIRSTSSKEIVHTPET 240  
 QY 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFQSDVQNPFPYNDINWDVAVFQKRLIPGIP 300  
 Db 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFQSDVQNPFPYNDINWDVAVFQKRLIPGIP 300  
 QY 301 NKGRINCDPTTELEEMILESPLHKKKRLAKKEMKDKCDSSQTCLLQEHLDVSQKEFI 360  
 Db 301 NKGRINCDPTTELEEMILESPLHKKKRLAKKEMKDKCDSSQTCLLQEHLDVSQKEFI 360  
 QY 361 IFNREKVNDRDNKRNPNALALQTKDPQVTNGQ 392  
 Db 361 IFNREKVNDRDNKRNPNALALQTKDPQVTNGQ 392

RESULT 4  
 US-10-254-869-2  
 ; Sequence 2, Application US/10254869  
 ; Patent No. 6653117  
 ; GENERAL INFORMATION:  
 ; APPLICANT: YE, Jane et al  
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
 ; TITLE OF INVENTION: THEREOF  
 ; FILE REFERENCE: CL001160DIV  
 ; CURRENT APPLICATION NUMBER: US/10/254,869  
 ; CURRENT FILING DATE: 2002-09-26  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 396  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 ; US-10-254-869-2

Query Match 95.2%; Score 2047; DB 4; Length 396;  
 Best Local Similarity 98.7%; Pred. No. 1e-187;  
 Matches 387; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60  
DB 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60  
QY 61 ERNEVRNVFKELQIMQGLEHFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120  
DB 61 ERNEVRNVFKELQIMQGLEHFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120  
QY 121 ETVKLFICELWALDYLNQRIIHRDMKPNILLDEHGHVHITDFNIAAMLPRETQITTT 180  
DB 121 ETVKLFICELWALDYLNQRIIHRDMKPNILLDEHGHVHITDFNIAAMLPRETQITTT 180  
QY 181 AGTRPYMAPEMFSSRKGAGYFAVDWWSLGVYAYELLGRPRYHRSSTSSKEIVHPTET 240  
DB 181 AGTRPYMAPEMFSSRKGAGYFAVDWWSLGVYAYELLGRPRYHRSSTSSKEIVHPTET 240  
QY 241 TVVTYPSAWSQEMVSLKLLLEPNDFQSFQSDVQNPFPYNDINWDAVFOKRLIPG 300  
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DB 301 NKGRINCDPTELEBEMILESPLHKKKRLAKKCKDSSQTCLLQEHLDVQKFEI 360  
QY 361 IFNREKVRNDFNKRQPNLALEQTKDPQVNTGQ 392  
DB 361 IFNREKVRNDFNKRQPNLALEQTKDPQGEDGQ 392

RESULT 5  
US-10-801-876B-4  
; Sequence 4, Application US/09801876B  
; Patent No. 6492155  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001160  
; CURRENT APPLICATION NUMBER: US/09/801,876B  
; CURRENT FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 404  
; TYPE: PRT  
; ORGANISM: Mus Musculus  
US-10-801-876B-4

Query Match 66.5%; Score 1430.5; DB 4; Length 404;  
Best Local Similarity 68.1%; Pred. No. 1.2e-128;  
Matches 280; Conservative 43; Mismatches 71; Indels 17; Gaps 5;  
QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60  
DB 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60  
QY 61 ERNEVRNVFKELQIMQGLEHFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 119  
DB 61 ERNEVRNVFKELQIMQGLEHFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFT 120  
QY 120 ETVKLFICELWALDYLNQRIIHRDMKPNILLDEHGHVHITDFNIAAMLPRETQITTT 179  
DB 121 EGTVKLYICELALALEYLQRYHIIHRDKPNDILLDEHGHVHITDFNIAATLVKSEKASS 180  
QY 180 MAGTKPYMAPEMFSSRKGAGYFAVDWWSLGVYAYELLGRPRYHRSSTSSKEIVHPT 237  
DB 181 MAGTKPYMAPEMFSSRKGAGYFAVDWWSLGVYAYELLGRPRYHRSSTSSKEIVHPT 240  
QY 238 FETTVVTYPSAWSQEMVSLKLLLEPNDFQSFQSDVQNPFPYNDINWDAVFOKRLIPG 297  
DB 241 FKVERVHYSSTWCEGWSLKKLLTKDPESLSLRDIQSMYTLADNMWDAVFEKALMPG 300

QY 298 FIPNKGRLNCDPTELEBEMILESPLHKKKRLAK-KEKDMRKCDSSQTCLLQEHLDVQ 356  
DB 301 FVPNKGRLNCDPTELEBEMILESPLHKKKRLAKHRSRSTKSCPLNGHLOQCLETVR 360  
QY 357 KEFTIFNREKVRNDFNKRQPNLALEQTKDPQVNTGQ 405  
DB 361 KEFTIFNREKVRNDFNKRQPNLALEQTKDPQVNTGQ 400  
RESULT 6  
US-10-254-865-4  
; Sequence 4, Application US/10254869  
; Patent No. 6653117  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001160DIV  
; CURRENT APPLICATION NUMBER: US/10/254,869  
; CURRENT FILING DATE: 2002-09-26  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 404  
; TYPE: PRT  
; ORGANISM: Mus Musculus  
US-10-254-865-4

Query Match 66.5%; Score 1430.5; DB 4; Length 404;  
Best Local Similarity 68.1%; Pred. No. 1.2e-128;  
Matches 280; Conservative 43; Mismatches 71; Indels 17; Gaps 5;  
QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60  
DB 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60  
QY 61 ERNEVRNVFKELQIMQGLEHFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 119  
DB 61 ERNEVRNVFKELQIMQGLEHFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFT 120  
QY 120 ETVKLFICELWALDYLNQRIIHRDMKPNILLDEHGHVHITDFNIAAMLPRETQITTT 179  
DB 121 EGTVKLYICELALALEYLQRYHIIHRDKPNDILLDEHGHVHITDFNIAATLVKSEKASS 180  
QY 180 MAGTKPYMAPEMFSSRKGAGYFAVDWWSLGVYAYELLGRPRYHRSSTSSKEIVHPT 237  
DB 181 MAGTKPYMAPEMFSSRKGAGYFAVDWWSLGVYAYELLGRPRYHRSSTSSKEIVHPT 240  
QY 238 FETTVVTYPSAWSQEMVSLKLLLEPNDFQSFQSDVQNPFPYNDINWDAVFOKRLIPG 297  
DB 241 FKVERVHYSSTWCEGWSLKKLLTKDPESLSLRDIQSMYTLADNMWDAVFEKALMPG 300  
QY 298 FIPNKGRLNCDPTELEBEMILESPLHKKKRLAK-KEKDMRKCDSSQTCLLQEHLDVQ 356  
DB 301 FVPNKGRLNCDPTELEBEMILESPLHKKKRLAKHRSRSTKSCPLNGHLOQCLETVR 360  
QY 357 KEFTIFNREKVRNDFNKRQPNLALEQTKDPQVNTGQ 405  
DB 361 KEFTIFNREKVRNDFNKRQPNLALEQTKDPQVNTGQ 400

RESULT 7  
US-09-801-876B-5  
; Sequence 5, Application US/09801876B  
; Patent No. 6492155  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001160

; CURRENT APPLICATION NUMBER: US/09/801.876B  
; CURRENT FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 403  
; TYPE: PRT  
; ORGANISM: Human  
US-09-801-876B-5

Query Match 66.2%; Score 1423.5; DB 4; Length 403;  
Best Local Similarity 72.3%; Pred. No. 5.4e-128;  
Matches 269; Conservative 40; Mismatches 60; Indels 3; Gaps 2;

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QY 1 MGANTSRKPPVFDNEDVNFDFHILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKCV 60
D 1 MGNHSHKPPVFDNEEVNFDFHILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKCI 60
61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEDMFMVVDLLGGDLRVHLOQNVHFE 120
61 ERDEVNRVPRELOIMQGLEHPPFLVNLWYSFQDEDMFMVVDLLGGDLRVHLOQNVHFE 120
121 ETVKLFICELVMDLYLQNOIRIHRDMKPDNILLDEGHVHITDFNIAAMLPRETOITTM 180
121 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEGHVHITDFNIAATVVGKGRASSM 180
181 AGTKPYMAPEMFS--SRKAGYSFVDMWSLGVTAPELLRGRPRPYHRSSTSSKEIVHTF 238
181 AGTKPYMAPEVQVYMDRGPYSPVDMWSLGVTAPELLRGRPRPYHRSVTPIDEILNMF 240
239 ETTVTVPYSAWSQEMVSLKLLKLEPNPDQRFSDVQNFPPYMDINWDVAFQKRLIPGF 298
241 KVERVHYSSTWCKGMVALLKLLTKDPESRVSSLDIQSVPYLADNMWDVAFKALMPGF 300
299 IPNKGRLNCPTPELEEMILESPLHKKKKRLAK-KEKDMRKCDSSQTCLLQEHLDVQK 357
301 VPNGRLNCPTPELEEMILESPLHKKKKRLAKNRSDGTGKDCPLNGHLQHCLETVRE 360
358 EFIIFNREKVR 369
361 EFIIFNREKLRR 372
```

RESULT 8

US-10-254-869-5  
; Sequence 5, Application US/10254869  
; Patent No. 6653117

GENERAL INFORMATION:

APPLICANT: YE, Jane et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CLO01160DIV

CURRENT APPLICATION NUMBER: US/10/254.869

CURRENT FILING DATE: 2002-09-26

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 403

TYPE: PRT

ORGANISM: Human

US-10-254-869-5

Query Match 66.2%; Score 1423.5; DB 4; Length 403;  
Best Local Similarity 72.3%; Pred. No. 5.4e-128;  
Matches 269; Conservative 40; Mismatches 60; Indels 3; Gaps 2;

```
QY 1 MGANTSRKPPVFDNEDVNFDFHILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKCV 60
D 1 MGNHSHKPPVFDNEEVNFDFHILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKCI 60
61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEDMFMVVDLLGGDLRVHLOQNVHFE 120
```

QY

D

QY

D

QY

D

```

; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-254-869-6

Query Match 61.8%; Score 1328.5; DB 4; Length 384;
Best Local Similarity 64.5%; Pred. No. 6.3e-119;
Matches 251; Conservative 55; Mismatches 74; Indels 9; Gaps 3;

QY 304 VPKGRLHCDPTELEEMILESPLHKKKRLAKNKRSDRSSQSENDYLOCDLAIQ 363
QY 357 KEFIIENREKVNDRFNALALEQTKD 385
Db 364 QDFVIENREKLSQDLPREPLPAPERD 392

RESULT 10
US-09-801-876B-6
; Sequence 6, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-801-876B-6

Query Match 61.8%; Score 1328.5; DB 4; Length 384;
Best Local Similarity 64.5%; Pred. No. 6.3e-119;
Matches 251; Conservative 55; Mismatches 74; Indels 9; Gaps 3;

QY 6 SRKPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCVNERV 65
Db 1 SARRPVFDDKEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCIERDEV 60
QY 66 RNVFKELIQMGLPEHFLVNLWYSFQDEDMVMVVDLLGGDLRYHLQONVHFKEETVKL 125
Db 61 RNVFRELEILOEIEHVFVNLWYSFQDEDMVMVVDLLGGDLRYHLQONVQFSEDIVRL 120
QY 126 FICELVMDLYLONKRIIHRDMKPNILLDEGHVHITDENIAAMLPRETOITTWAGTKP 185
Db 121 YICEMALDYLRSQHIIHRDVKPNILLDEQGAHLTDNFNIIKQGERATALAGTKP 180
QY 186 YMAPEMFSS--RKGAGYFAVDWNSLGVATAYELLRGRPRPYHRSSTSSKEIVHTPETTV 243
Db 181 YMAPEIFHSFVNGGTGYSGFEVDWNSVGMAYELLRGRPRPYDIHSSNAVESLVQLESTVS 240
QY 244 TYPNSWSEMSYLLKLEPNPDQRFSDVQNPYPYNDINWDVAFQKRLIPGIPNKG 303
Db 241 QYVPTWSKEMVALLRKLTVNPEHRFSSLDQMOTAPSLAHVLWDLSEKKVPEGFPVNGK 300
QY 304 RLNCDPTELEEMILESPLHKKKRLAKKEMKCDSSOT--CLLOEHLDSVQKEFII 361
Db 301 RLHCDPTELEEMILESPLHKKKRLAKNKRSDRSSQSENDYLOCDLAIQDFVI 360
QY 362 FNREKVNDRFNKRONLALEQTKDPQVTN 390
Db 361 FNREKLI-----KRSQELMSEPPPGPETS 384

RESULT 11
US-10-254-869-6
; Sequence 6, Application US/10254869
; Patent No. 6653117
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160DIV
; CURRENT APPLICATION NUMBER: US/10/254,869
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-819-607-4

Query Match 60.2%; Score 1294.5; DB 4; Length 399;
Best Local Similarity 63.4%; Pred. No. 1.2e-115;
Matches 248; Conservative 54; Mismatches 80; Indels 9; Gaps 3;

QY 18 VNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCVNERVNVFKELIQMQG 77
Db 1 VNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCIERDEVNVFRELEILOE 60
QY 78 LEHPFLVNLWYSFQDEDMVMVVDLLGGDLRYHLQONVHFKEETVKLFCLELWALDYL 137
Db 61 IEHVFVNLWYSFQDEDMVMVVDLLGGDLRYHLQONVQFSEDIVRLYICEMALDYL 120
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; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-254-869-6

Query Match 61.8%; Score 1328.5; DB 4; Length 384;
Best Local Similarity 64.5%; Pred. No. 6.3e-119;
Matches 251; Conservative 55; Mismatches 74; Indels 9; Gaps 3;

QY 5 SRKPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCVNERV 65
Db 1 SARRPVFDDKEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCIERDEV 60
QY 65 RNVFKELIQMGLPEHFLVNLWYSFQDEDMVMVVDLLGGDLRYHLQONVHFKEETVKL 125
Db 61 RNVFRELEILOEIEHVFVNLWYSFQDEDMVMVVDLLGGDLRYHLQONVQFSEDIVRL 120
QY 125 FICELVMDLYLONKRIIHRDMKPNILLDEGHVHITDENIAAMLPRETOITTWAGTKP 185
Db 121 YICEMALDYLRSQHIIHRDVKPNILLDEQGAHLTDNFNIIKQGERATALAGTKP 180
QY 186 YMAPEMFSS--RKGAGYFAVDWNSLGVATAYELLRGRPRPYHRSSTSSKEIVHTPETTV 243
Db 181 YMAPEIFHSFVNGGTGYSGFEVDWNSVGMAYELLRGRPRPYDIHSSNAVESLVQLESTVS 240
QY 244 TYPNSWSEMSYLLKLEPNPDQRFSDVQNPYPYNDINWDVAFQKRLIPGIPNKG 303
Db 241 QYVPTWSKEMVALLRKLTVNPEHRFSSLDQMOTAPSLAHVLWDLSEKKVPEGFPVNGK 300
QY 304 RLNCDPTELEEMILESPLHKKKRLAKKEMKCDSSOT--CLLOEHLDSVQKEFII 361
Db 301 RLHCDPTELEEMILESPLHKKKRLAKNKRSDRSSQSENDYLOCDLAIQDFVI 360
QY 362 FNREKVNDRFNKRONLALEQTKDPQVTN 390
Db 361 FNREKLI-----KRSQELMSEPPPGPETS 384

RESULT 12
US-09-819-607-4
; Sequence 4, Application US/09819607
; Patent No. 6686176
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001078
; CURRENT APPLICATION NUMBER: US/09/819,607
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-819-607-4

Query Match 60.2%; Score 1294.5; DB 4; Length 399;
Best Local Similarity 63.4%; Pred. No. 1.2e-115;
Matches 248; Conservative 54; Mismatches 80; Indels 9; Gaps 3;

QY 18 VNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCVNERVNVFKELIQMQG 77
Db 1 VNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCIERDEVNVFRELEILOE 60
QY 78 LEHPFLVNLWYSFQDEDMVMVVDLLGGDLRYHLQONVHFKEETVKLFCLELWALDYL 137
Db 61 IEHVFVNLWYSFQDEDMVMVVDLLGGDLRYHLQONVQFSEDIVRLYICEMALDYL 120
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QY 138 QNQRILHRDKPDNILLDEGHVHITDPTNIAAMLPRETOITTMAGTGYPMAPMFSS-R 195  
Db 121 RSQHIIHRDKPDNILLDEGHVHITDPTNIAAMLPRETOITTMAGTGYPMAPMFSS-FVN 180  
QY 196 KGAGYSPAVDWSLGVATAYELLRRRRYHRSSTSSKEIVHTPTTIVVTYPSAWSQBMWS 255  
Db 181 GGTGYSEVDWSVGVWVAYELLRGWRBYDIHSSNAVESLVQLFSTVSQVQVPTWSKEMVA 240  
QY 256 LKLLLEPNDRPQSLSVDQNFYPMNDINWDVQKRLIPGFIPNKGRLNCDPTFLEE 315  
Db 241 LLRLKLLTVNPEHRPSSLDQMCTAPSLAHVLWDLSEKKVEPGFVFNKGRGLHCDPTFLEE 300  
QY 316 MILESKEPLHKKKELAKEXDKMRKDCSSQT--CLLOHLSVQKEFTIENREKVNRFNK 373  
Db 301 MILESRLPHKKKRLAKNKSRSRDSQSENDVYQCLDAIQDFVFNREKL-----K 355  
QY 374 ROPNLALEQTKDPQVINGQMDTGLSETFQTS 404  
Db 356 RSQELMSEPPPGPPTSDMTDSTADSEAEPTA 396

## RESULT 13

US-09-841-683-7  
; Sequence 7, Application US/09841683  
; Patent No. 6617147  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Yi  
; APPLICANT: Nepomniichy, Boris  
; APPLICANT: Wang, Xiaoming  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Scoville, John  
; APPLICANT: Walke, D. Wade  
; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding  
; FILE REFERENCE: LEX-0167-USA  
; CURRENT APPLICATION NUMBER: US/09/841,683  
; PRIOR FILING DATE: 2001-04-24  
; PRIOR APPLICATION NUMBER: US 60/199,499  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: US 60/201,227  
; PRIOR FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-841-683-7

Query Match 54.6%; Score 1174; DB 4; Length 236;  
Best Local Similarity 91.1%; Pred. No. 2e-104;  
Matches 224; Conservative 1; Mismatches 1; Indels 20; Gaps 1;

QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKV 60  
Db 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKV 60  
QY 61 ERNEVERNFKELIQMOGLEHPLVNLWYSQDEDMFMVVDLLGGDLRYHLOQNVHFXE 120  
Db 61 ERNEVERNFKELIQMOGLEHPLVNLWYSQDEDMFMVVDLLGGDLRYHLOQNVHFXE 120  
QY 121 ETVKLFICELVWALDYLNQRIIHRDKPDNILLDEGHVHITDPTNIAAMLPRETOITTM 180  
Db 121 ETVKLFICELVWALDYLNQRIIHRDKPDNILLDEGHVHITDPTNIAAMLPRETOITTM 180  
QY 181 AGTKPYMAPMFSSRRKGAGYSFAVDWWSLGVATAYELLRGR 240  
Db 181 AGTKPYMAPMFSSRRKGAGYSFAVDWWSLGVATAYELLRGR 240

RESULT 14  
US-09-841-683-5  
; Sequence 5, Application US/09841683  
; Patent No. 6617147  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Yi  
; APPLICANT: Nepomniichy, Boris  
; APPLICANT: Wang, Xiaoming  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Scoville, John  
; APPLICANT: Walke, D. Wade  
; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding  
; FILE REFERENCE: LEX-0167-USA  
; CURRENT APPLICATION NUMBER: US/09/841,683  
; CURRENT FILING DATE: 2001-04-24  
; PRIOR APPLICATION NUMBER: US 60/199,499  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: US 60/201,227  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 225  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-841-683-5

Query Match 54.4%; Score 1171; DB 4; Length 225;  
Best Local Similarity 100.0%; Pred. No. 3.5e-104;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKV 60  
Db 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKV 60  
QY 61 ERNEVERNFKELIQMOGLEHPLVNLWYSQDEDMFMVVDLLGGDLRYHLOQNVHFXE 120  
Db 61 ERNEVERNFKELIQMOGLEHPLVNLWYSQDEDMFMVVDLLGGDLRYHLOQNVHFXE 120  
QY 121 ETVKLFICELVWALDYLNQRIIHRDKPDNILLDEGHVHITDPTNIAAMLPRETOITTM 180  
Db 121 ETVKLFICELVWALDYLNQRIIHRDKPDNILLDEGHVHITDPTNIAAMLPRETOITTM 180  
QY 181 AGTKPYMAPMFSSRRKGAGYSFAVDWWSLGVATAYELLRGR 220  
Db 181 AGTKPYMAPMFSSRRKGAGYSFAVDWWSLGVATAYELLRGR 220

RESULT 15  
US-09-819-607-2  
; Sequence 2, Application US/09819607  
; Patent No. 6686176  
; GENERAL INFORMATION:  
; APPLICANT: BEASLEY, Ellen et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THERSOF  
; FILE REFERENCE: CL001078  
; CURRENT APPLICATION NUMBER: US/09/819,607  
; CURRENT FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 369  
; TYPE: PRT  
; ORGANISM: Human  
US-09-819-607-2

Query Match 53.1%; Score 1142; DB 4; Length 369;  
Best Local Similarity 63.2%; Pred. No. 4.3e-101;  
Matches 216; Conservative 50; Mismatches 72; Indels 4; Gaps 2;

QY 43 MYAMKYNKQKCVNERNEVNFKELIQMOGLEHPLVNLWYSQDEDMFMVVDLLGGD 107

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1 MYAMKYNKQOCIERDEVNRFRELEIQEIEHVFVLNLTWYSFQDEEDMFVVDLLGGD 60
108 LRYHLQONVHFKEETVKLFCICELVMDYLQONRIIHRDMKPDNILLDEHGHVHTDFNI 167
61 LRYHLQONVQSEDTVRLYICEMALADYLRGQHIHRDVKPDNILLDERGHAHLTDFNI 120
168 AAMPLPRETOITMAGTKPYMAPEMFSS--RKGAGYSFAVDWMSLGVYAYELLRGRPYHI 225
121 ATIIKDGGERATALAGTKPYMAPEIFHSPVNGGTGYSFEVDWMSVGVWAYELLRGWRPYDI 180
226 RSSTSSKEIVHTEETTVVTPSAMQEMVSLKLLBNPDORFSQLSDYQNFYMDIN 285
181 HSSNAVESLVOLFSTVSQYVPTWSKEMVALLRKLITVNPHEHRLSSLDQVQAPALAGVL 240
286 WDAVFQKRLIFGFIPNKGRLNCDPTFELEEMILESXPLHKKKKLAKKEDMRKCDSSQT 345
241 WDHLSEKRVFPGFVPNKGRLHCDPTFELEEMILESRLHKKKKLAKKEDMRKCDSSQS 300
346 --CLLOEHLDVQKEFIIFNREKVNROFNKQPNALAEQTKD 385
301 ENDYLODCLDAIQODFVIFNREKLKRSQDLPREPLPAPESRD 342

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Search completed: May 26, 2004, 20:20:56  
Job time : 24 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 26, 2004, 20:15:03 ; Search time 45 Seconds  
(without alignments)  
2853.687 Million cell updates/sec

Title: US-10-620-845-9

Perfect score: 2151

Sequence: 1 MGANTSRRPPVDENEDVNF.....VTNGQMDTGLSETFQTSKVS 407

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Sequenced: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SETPREMBL 25:\*

1: sp archaea:\*

2: sp bacteria:\*

3: sp fungi:\*

4: sp human:\*

5: sp invertebrate:\*

6: sp mammal:\*

7: sp mhc:\*

8: sp organelle:\*

9: sp phage:\*

10: sp plant:\*

11: sp rodent:\*

12: sp virus:\*

13: sp vertebrate:\*

14: sp unclassified:\*

15: sp virus:\*

16: sp bacteriaph:\*

17: sp archaheap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1880	87.4	398	11 Q8BGW6	Q8BGW6 mus musculus
2	1707	79.4	368	11 Q7TPQ4	Q7TPQ4 mus musculus
3	1441	67.0	414	11 Q3JUX8	Q3JUX8 mus musculus
4	1438.5	66.9	414	11 Q7TMD3	Q7TMD3 mus musculus
5	1434.5	66.7	414	11 Q8C4E0	Q8C4E0 mus musculus
6	1423.5	66.2	414	4 Q9NY57	Q9NY57 homo sapien
7	1419.5	66.0	414	4 Q81Y14	Q81Y14 homo sapien
8	1333.5	62.0	488	11 Q87JG4	Q87JG4 mus musculus
9	1333.5	62.0	488	11 Q8QZV4	Q8QZV4 mus musculus
10	1332.5	61.9	486	4 Q86UX6	Q86UX6 homo sapien
11	1142	53.1	369	4 Q96BA3	Q96BA3 homo sapien
12	1142	53.1	369	4 Q8GUE1	Q8GUE1 homo sapien
13	1127.5	52.4	368	6 Q9BGT4	Q9BGT4 macaca fasc
14	852.5	39.6	379	5 Q21483	Q21483 caenorhabdi
15	835	38.8	166	4 Q8WU08	Q8WU08 homo sapien
16	714.5	33.2	700	5 Q9VN23	Q9VN23 drosophila

## ALIGNMENTS

### RESULT 1

ID	Q8BGW6	PRELIMINARY;	PRT;	398 AA.
AC	Q8BGW6;			
DT	01-MAR-2003 (Tremblrel. 23, Created)			
DT	01-MAR-2003 (Tremblrel. 23, Last sequence update)			
DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)			
DE	Similar to serine threonine kinase 32 homolog.			
GN	A930015H13RIK.			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;			
RX	MEDLINE=23154683; PubMed=12466851;			
RA	The FANTOM Consortium,			
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;			
RT	"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."			
RL	Nature 420:563-573 (2002).			
DR	EMBL; AK036266; BAC31302.1; --			
DR	EMBL; AK044474; BAC31941.1; --			
DR	MGI; MGI:2442403; A330015B13RIK.			
DR	GO; GO:0005524; F:ATP binding; IEA.			
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.			
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.			
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.			
DR	InterPro; IPR000719; Prot.kinase.			
DR	InterPro; IPR002290; Ser_thr_kinase.			
DR	InterPro; IPR008271; Ser_thr_pkin_AS.			
DR	Pfam; PF00069; pkinase; 1.			
DR	PRINTS; PR00109; TYRKINASE.			
DR	ProDom; PD000001; Prot.kinase; 1.			
DR	SMART; SM00220; S_TKc; 1.			
DR	SMART; SM00219; TyrKc; 1.			

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 SQ SEQUENCE 398 AA; 46509 MW; 689BCA5B25CF18BB CRC64;

Query Match 87.4%; Score 1880; DB 11; Length 398;  
 Best Local Similarity 91.2%; Pred. No. 9.5e-145;  
 Matches 351; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVOKNDTKMYAMKYNKQKCV 60  
 DB 1 MGANTSSKAPVFDENEDVNFDFEILRAIGKSGFGKVCIVOKNDTKMYAMKYNKQKCV 60

QY 61 ERNEVRNVFKELQIMOGLHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFE 120  
 DB 61 ERNEVRNVFKELQIMOGLHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFE 120

QY 121 ETVKLFICELVMDLYLQNKRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTM 180  
 DB 121 DTVKLFICELVMDLYLQNKRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTV 180

QY 181 AGTKPYMAPEMFSSKRGAGYSFAVDWNSLGVATYELLGRRPYHRSSTSSKEIVHTPET 240  
 DB 181 AGTKPYMAPEMFTSRKETGYSFVADWNSLGVATYELLGRRPYHRSSTSSKEIVNMFT 240

QY 241 TVVTYPSAWSQEMVSLIKLLEPNPDQFSPQSLSVQNPFPYNDINWDAVFOKRLIPGIP 300  
 DB 241 AIVTYPSAWSQEMVSLIKLLEPNPDQFSPQSLSVQNPFPYNDINWDAVFOKRLIPGIP 300

QY 301 NKGRINCNDPTFELEEMILESKPLHKKKRLAKKEMKCDSSOTCLLOEHLDSVQKEFI 360  
 DB 301 TKGRINCNDPTFELEEMILESKPLHKKKRLAKKEMKCDSSOTCLLOEHLDAVQKEFI 360

QY 361 IFNREKVNDRDFNKRQPNLALEQTKD 385  
 DB 361 IFNREKVKSDFNQRQANLALEQTKN 385

RESULT 2  
 ID Q7TPQ4 PRELIMINARY; PRT; 368 AA.  
 Q7TPQ4:  
 01-OCT-2003 (TRENBLrel. 25, Created)  
 01-OCT-2003 (TRENBLrel. 25, Last sequence update)  
 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 Hypothetical protein.  
 Mus musculus (Mouse).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 SEQUENCE FROM N.A.  
 TISSUE=Olfactory epithelium;  
 MEDLINE=22389257; PubMed=12477932;  
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Haieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulliahy S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 Jones S.J., Marra M.A.;  
 "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Olfactory epithelium;  
 RA Strausberg R.;  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC055002; AAH55002.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 368 AA; 43213 MW; 0DB7F6977C39BB56 CRC64;

Query Match 79.4%; Score 1707; DB 11; Length 368;  
 Best Local Similarity 84.2%; Pred. No. 1e-130;  
 Matches 324; Conservative 17; Mismatches 14; Indels 30; Gaps 1;

QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVOKNDTKMYAMKYNKQKCV 60  
 DB 1 MGANTSSKAPVFDENEDVNFDFEILRAIGKSGFGKVCIVOKNDTKMYAMKYNKQKCV 60

QY 61 ERNEVRNVFKELQIMOGLHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFE 120  
 DB 61 ERNEVRNVFKELQIMOGLHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFE 120

QY 121 ETVKLFICELVMDLYLQNKRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTM 180  
 DB 121 DTVKLFICELVMDLYLQNKRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTV 180

QY 181 AGTKPYMAPEMFSSKRGAGYSFAVDWNSLGVATYELLGRRPYHRSSTSSKEIVHTPET 240  
 DB 181 AGTKPYMAPEMFTSRKETGYSFVADWNSLGVATYELLGRRPYHRSSTSSKEIVNMFT 240

QY 241 TVVTYPSAWSQEMVSLIKLLEPNPDQFSPQSLSVQNPFPYNDINWDAVFOKRLIPGIP 300  
 DB 241 AIVTYPSAWSQEMVSLIKLLEPNPDQFSPQSLSVQNPFPYNDINWDAVFOKRLIPGIP 300

QY 301 NKGRINCNDPTFELEEMILESKPLHKKKRLAKKEMKCDSSOTCLLOEHLDSVQKEFI 360  
 DB 301 TKGRINCNDPTFELEEMILESKPLHKKKRLAKKEMKCDSSOTCLLOEHLDAVQKEFI 360

QY 361 IFNREKVNDRDFNKRQPNLALEQTKD 385  
 DB 361 IFNREKVKSDFNQRQANLALEQTKN 385

RESULT 3  
 ID Q9JJK8 PRELIMINARY; PRT; 414 AA.  
 Q9JJK8:  
 AC Q9JJK8:  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Serine/threonine protein kinase.  
 GN STX32.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20164328; PubMed=10700184;  
 RA Ruiz-Perez V.L., Ide S.E., Strom T.M., Lorenz B., Wilson D., Woods K.,  
 King L., Francmann C., Freisinger P., Spranger S., Marino B.,  
 Dallapiccola B., Wright M., Meitinger T., Polymeropoulos M.H.,  
 Goodship J.;  
 RT "Mutations in a new gene in Ellis-van Creveld syndrome and Webers  
 acrocardial dysostosis";  
 RL Nat. Genet. 24:283-286 (2000).  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; AJ250840; CAB76566.1; -;  
 DR HSP3; P05132; 1CTP.  
 DR MGD; MGI:1927552; Stk32.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.



GO: G0:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro: IPR000719; Prot kinase.  
 DR InterPro: IPR002290; Ser chr\_pkinase.  
 DR InterPro: IPR008271; Ser\_chr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1  
 DR ProDom: PD000001; Prot\_kinase; 1.  
 DR SMART: SMC0220; S\_TKc; 1.  
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.  
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 414 AA; 47917 MW; BE394415790B9A13 CRC64;

Query Match 67.0%; Score 1441; DB 11; Length 414;  
 Best Local Similarity 68.3%; Pred. No. 5.5e-109;  
 Matches 280; Conservative 43; Mismatches 71; Indels 16; Gaps 4;

QY 1 MGANTSRRKPPVDFEDNEVDNFDHPEILRAIGKSGFGKVCIVQKNDTKWYAMKYNKQKV 60  
 DB 1 MGNHSHKPPVDFEDNEVDNFDHPEILRAIGKSGFGKVCIVQKNDTKWYAMKYNKQKV 60  
 QY 61 ERNEVRNVFRELQIMQGLEHPPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFKE 120  
 DB 61 ERDEVRNVFRELQIMQGLEHPPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFTE 120  
 QY 121 ETVKLFICELVMDLYLQONRIHRDMKPNILLDEGHVHITDFNIAAMLPRETQITTM 180  
 DB 121 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEGHVHITDFNIAATVLKSGEKASS 180  
 QY 181 AGTPYMAPEMFS--SRKGAGYFAVDWWSLGVAYELLRGRRPYHRSSTSSKEIVHTF 238  
 DB 181 AGTPYMAPEVQVYVVGPGFGYSPVWWSLGVAYELLRGRRPYHRSSTSSKEIVHTF 240  
 QY 239 ETTVVTVPSAWSQEMVSLKLLKLEPNPDQFSQLSDVQNFYPMNDINWDVAFQKRLIPGF 298  
 DB 241 KVERVHVSSTWCEGWSLLKLLTKDPESRLSSLDIQSTYTLADNMWDVAFKALMPGF 300  
 QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKKLAK-KEKDMKCDSSQTCLLQOEHLDSVQK 357  
 DB 301 VPNGRLNCDPTFELEEMILESPLHKKKKLAKHRSRDSSTKDSCLNGHLQOCLTVRK 360  
 QY 358 EFILFNREKVRDNFKRQPNLALEQTKDPQVT--NGQMDTGLSETFQSK 405  
 DB 361 EFILFNREKLRR-----OQGHGOLSLDGRIGTSSTKLQDGR 399

RESULT 4  
 QY Q7TMD3 PRELIMINARY; PRT; 414 AA.  
 DB Q7TMD3;  
 DT 01-OCT-2003 (TremBLrel. 25, Created)  
 DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=22389257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner K.H., Schefer C.F., Bhat N.K.,  
 RA Altachul S.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshyunski S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Kzyvinski M.I., Skalska J., Smalusz D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RA Strausberg R.;  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC052404; AAH52404.1; -;  
 DR EMBL; BC056396; AAH56396.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 414 AA; 47916 MW; 3C394415790594F3 CRC64;

Query Match 66.9%; Score 1438.5; DB 11; Length 414;  
 Best Local Similarity 70.2%; Pred. No. 8.8e-109;  
 Matches 278; Conservative 36; Mismatches 63; Indels 19; Gaps 3;

QY 1 MGANTSRRKPPVDFEDNEVDNFDHPEILRAIGKSGFGKVCIVQKNDTKWYAMKYNKQKV 60  
 DB 1 MGNHSHKPPVDFEDNEVDNFDHPEILRAIGKSGFGKVCIVQKNDTKWYAMKYNKQKV 60  
 QY 61 ERNEVRNVFRELQIMQGLEHPPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFKE 120  
 DB 61 ERDEVRNVFRELQIMQGLEHPPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFTE 120  
 QY 121 ETVKLFICELVMDLYLQONRIHRDMKPNILLDEGHVHITDFNIAAMLPRETQITTM 180  
 DB 121 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEGHVHITDFNIAATVLKSGEKASS 180  
 QY 181 AGTPYMAPEMFS--SRKGAGYFAVDWWSLGVAYELLRGRRPYHRSSTSSKEIVHTF 238  
 DB 181 AGTPYMAPEVQVYVVGPGFGYSPVWWSLGVAYELLRGRRPYHRSSTSSKEIVHTF 240  
 QY 239 ETTVVTVPSAWSQEMVSLKLLKLEPNPDQFSQLSDVQNFYPMNDINWDVAFQKRLIPGF 298  
 DB 241 KVERVHVSSTWCEGWSLLKLLTKDPESRLSSLDIQSTYTLADNMWDVAFKALMPGF 300  
 QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKKLAK-KEKDMKCDSSQTCLLQOEHLDSVQK 357  
 DB 301 VPNGRLNCDPTFELEEMILESPLHKKKKLAKHRSRDSSTKDSCLNGHLQOCLTVRK 360  
 QY 358 EFILFNREKVRDNFKRQPNLALEQTKDPQVTNGQM 393  
 DB 361 EFILFNREKLRRQ-----OQHGQL 380

RESULT 5  
 QY Q8C4E0 PRELIMINARY; PRT; 414 AA.  
 DB Q8C4E0;  
 DT 01-MAR-2003 (TremBLrel. 23, Created)  
 DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)  
 DE Serine threonine kinase 32.  
 GN STK32.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

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RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK082468; BAC38500.1; -.
DR MGD; MGI:1927552; Stk32.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
SQ SEQUENCE 414 AA; 47884 MW; 9C394364BE19E945 CRC64;
Query Match 66.7%; Score 1434.5; DB 11; Length 414;
Best Local Similarity 69.9%; Pred. No. 1.9e-108;
Matches 277; Conservative 37; Mismatches 63; Indels 19; Gaps 3;
QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKKVMYAMKYNKQKV 60
DB 1 MGNHSHKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKKVMYAMKYNKQKV 60
QY 61 ERNEVRNVKLEIQMGLHPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQNVHFKE 120
DB 61 ERDEVNRFELIQMGLHPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQNVHFTE 120
QY 121 ETVKLFICELVMDLYQNRITHRDMKPDNILLDEHGHVHTDFNIAAMLPRETOITWM 180
DB 121 GTVKLYICELALALEYQRYHITHRDIPKPDNILLDEHGHVHTDFNIAATVKGSEKASV 180
QY 181 AGTKPYMAPEMFS--SRKAGAGYFVADWWSLGVYAVELLGRPPYHTRSTSSKEIVHTF 238
DB 181 AGTKPYMAPEVQYVVDGGGYSYPVDWWSLGVYAVELLGRPPYHTRSTSSKEIVHTF 240
QY 239 ETTVTVPYSAWSQEMVSLKLLKLEPNPDQRFSDVQNPFPYNDINWDVAFQKRLIPGF 298
DB 241 KVERVHYSSTWCGWVSLAKLLTKDPESSLRDIQSMYTLADNMWDVAFKALMPGF 300
QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKKRLAK-KEKDMRKCDSSQTCLLQHLDSVQK 357
DB 301 VPNGKRLNCDPTFELEEMILESPLHKKKKRLAKRSRSTKDCSPLNGHLQCLQETVRK 360
QY 358 EFTIFNREKVRNDRFNKQPNLALEQTKDPQVINGQM 393
DB 361 EFTIFNREKVRNDRFNKQPNLALEQTKDPQVINGQM 393
RESULT 6
Q9NV57 PRELIMINARY; PRT; 414 AA.
AC Q9NV57;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Serine/threonine protein kinase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;

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RX MEDLINE=20164328; PubMed=10700184;
RA Ruiz-Perez V.L., Ide S.E., Strom T.M., Lorenz B., Wilson D., Woods K.,
RA King L., Francomano C., Freisinger P., Spranger S., Marino B.,
RA Dallapiccola B., Wright M., Meitinger T., Polymopoulos M.H.,
RA Goodship J.;
RT "Mutations in a new gene in Ellis-van Creveld syndrome and Weyers
RT acrorenal dysostosis.";
RL Nat. Genet. 24:283-286 (2000).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AJ250839; CAB76471.1; -.
DR HSSP; P05132; ICTP.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 414 AA; 47883 MW; 8FCD58A67EF09B0E CRC64;
Query Match 66.2%; Score 1423.5; DB 4; Length 414;
Best Local Similarity 72.3%; Pred. No. 1.5e-107;
Matches 269; Conservative 40; Mismatches 60; Indels 3; Gaps 2;
QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKKVMYAMKYNKQKV 60
DB 1 MGNHSHKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKKVMYAMKYNKQKV 60
QY 61 ERNEVRNVKLEIQMGLHPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQNVHFKE 120
DB 61 ERDEVNRFELIQMGLHPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQNVHFTE 120
QY 121 ETVKLFICELVMDLYQNRITHRDMKPDNILLDEHGHVHTDFNIAAMLPRETOITWM 180
DB 121 GTVKLYICELALALEYQRYHITHRDIPKPDNILLDEHGHVHTDFNIAATVKGSEKASV 180
QY 181 AGTKPYMAPEMFS--SRKAGAGYFVADWWSLGVYAVELLGRPPYHTRSTSSKEIVHTF 238
DB 181 AGTKPYMAPEVQYVVDGGGYSYPVDWWSLGVYAVELLGRPPYHTRSTSSKEIVHTF 240
QY 239 ETTVTVPYSAWSQEMVSLKLLKLEPNPDQRFSDVQNPFPYNDINWDVAFQKRLIPGF 298
DB 241 KVERVHYSSTWCGWVSLAKLLTKDPESSLRDIQSMYTLADNMWDVAFKALMPGF 300
QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKKRLAK-KEKDMRKCDSSQTCLLQHLDSVQK 357
DB 301 VPNGKRLNCDPTFELEEMILESPLHKKKKRLAKRSRSTKDCSPLNGHLQCLQETVRK 360
QY 358 EFTIFNREKVRNDRFNKQPNLALEQTKDPQVINGQM 393
DB 361 EFTIFNREKVRNDRFNKQPNLALEQTKDPQVINGQM 393
RESULT 7
Q8YI14 PRELIMINARY; PRT; 414 AA.
AC Q8YI14;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gene for serine/threonine protein kinase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;

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RC SEQUENCE FROM N.A.
RA TISSUE=Brain;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RM EMBL; BC038238; AAH38238.1; --
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr kinase.
DR InterPro; IPR008271; Ser Thr pkin_AS.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
KW Kinase; Serine/threonine-protein kinase.
SQ SEQUENCE 414 AA; 47784 MW; F05E8E95FA8242F CRC64;

Query Match 66.0%; Score 1419.5; DB 4; Length 414;
Best Local Similarity 72.3%; Pred. No. 3.1e-107;
Matches 269; Conservative 39; Mismatches 61; Indels 3; Gaps 2;

1 MGANTSRKPPVDEEDVNFDFEILRAIGKSGFGKVCIVQKNDTKQVAMKYNKQKCV 60
1 MGNHSHKPPVDEEDVNFDFEILRAIGKSGFGKVCIVQKNDTKQVAMKYNKQKCI 60
61 ERNEVRNFKELQIMQGLEHPEFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFK 120
61 ERDEVRNPRELQIMQGLEHPEFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFE 120
121 ETVKLFICELVMDLYLQNRILHRDMKPDNILLDEHGHVHITDNIAMLPRETQITTM 180
121 GTVKLYICELALALEYLRQYHILHRDIKPDNILLDEHGHVHITDNIAMLPVGAERASM 180
181 AGTKPMAPEMFS--SRKGAGYSFVDMWSLGVATYELLRGRPRYHIRSTSSKEIVHVF 238
181 AGTKPMAPEVQVYMDGSGYSFVDMWSLGVATYELLRGRPRYHIRSTSSKEIVHVF 240
239 ETVVTVPSAWQEMVSLKLLLEPNPDQRFQSLSDVQNPFPYNDINMDAVFQKLIPOF 298
241 KVERVHYSSTCKGMVALLKLLTKDPSRSVSLHDIQSPVYLADNMWDAVEKALMPGF 300
299 IPNKGRLNCDPTFELEEMILESKPLHKKKRLAK-KEKDMRKCDSSQTCILQEHLDVQK 357
301 VPKGRLNCDPTFELEEMILESKPLHKKKRLAKNRSDGTCKDSCPLNGHLQCLTVKE 360
358 EPIIFNREKVR 369
361 EPIIFNREKLR 372

RESULT 8
Q9JUG4 PRELIMINARY; PRT; 488 AA.
AC Q9JUG4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Brain cDNA, clone MNCB-1563, similar to A250840 serine/threonine
DE protein kinase (Mus musculus).
DE PAB.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;

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RA Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,
RA Hashimoto K.; Isolation of full-length cDNA clones from mouse brain cDNA library
RT made by oligo-capping method."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB041542; BAA95027.1; --
DR HSSP; F05132; ICTP.
DR MGD; MG-2385336; Pke.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr pkin_AS.
DR InterPro; IPR008271; Ser Thr pkin_AS.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 488 AA; 55276 MW; 310483FF69E24E39 CRC64;

Query Match 62.0%; Score 1333.5; DB 11; Length 488;
Best Local Similarity 63.3%; Pred. No. 3.8e-100;
Matches 255; Conservative 56; Mismatches 83; Indels 9; Gaps 3;

5 SEKPPVDEEDVNFDFEILRAIGKSGFGKVCIVQKNDTKQVAMKYNKQKCV 65
77 SARREVFDDKEDVNFDFEILRAIGKSGFGKVCIVQKNDTKQVAMKYNKQKCI 136
65 RNVFKELQIMQGLEHPEFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKETVKL 125
137 RNVFRELILQIEHPEFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFE 196
125 FICELVMDLYLQNRILHRDMKPDNILLDEHGHVHITDNIAMLPRETQITWAGTKP 185
197 YICENALDYLRSQHILHRDVKPDNILLDEGHVHITDNIATIKGGERATAGTKP 256
185 YNAPEMFS--RKGAGYSFVDMWSLGVATYELLRGRPRYHIRSTSSKEIVHVF 243
257 YNAPEIFHSFVNGGSGYSFVDMWSVGNVAYELLRGRPYDTHSSNAVESLQLESTVS 316
244 TYPSSAWSQEMVSLKLLLEPNPDQRFQSLSDVQNPFPYNDINMDAVFQKLIPIKNG 303
317 QVPTWSKEMVALLKLLTVNPEHRSLSLQDMQTPSLAHVLDLSEKKVEFGFVNKG 376
304 RLNCPTFELEEMILESKPLHKKKRLAKKEKDMRKCDSSQTCILQEHLDVQKEFII 361
377 RLHCDPTFELEEMILESKPLHKKKRLAKNRSDSSQSENNDYLDCLDAIQDFVI 436
362 FNRKVRNDRFKQPNLALQTKDPQVINGQMDTCGLSETFQTS 404
437 FNRKLR-----KRSQELMSPPPGTSDMTDSTADSEAPTA 474

RESULT 9
Q8QZV4 PRELIMINARY; PRT; 488 AA.
AC Q8QZV4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical serine/threonine protein kinase.
DE Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;

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Strausberg R.;  
Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
[2]  
SEQUENCE FROM N.A.  
STRAIN=C57BL/6J; TISSUE=Brain;  
MEDLINE=22354683; PubMed=12466851;  
The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs";  
RL Nature 420:563-573 (2002).  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL; BC026457; AH26457.1; -;  
DR EMBL; AK046439; BAC32730.1; -;  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0004688; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR002290; Ser Thr kinase.  
DR InterPro; IPR008271; Ser Thr\_pkin\_AS.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Prot kinase; 1.  
DR SMART; SM00220; S\_TKC; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW Hypothetical protein; ATP-binding; Kinase;  
KW Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 498 AA; 55262 MW; 296A927BE6B78E2 CRC64;  
Query Match 62.0%; Score 1333.5; DB 11; Length 488;  
Best Local Similarity 63.3%; Pred. No. 3.8e-100;  
Matches 255; Conservative 56; Mismatches 83; Indels 9; Gaps 3;  
6 SRKPPVDEDEDVNFDFHFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKVERNEV 65  
77 SARPPVDDKEDVNFDFHFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKQCIERDEV 136  
66 RNVPKEIQIMQGLEHPEFLVNLWYSFQDEDMFVVDLLGGLRLYHLQNVHFEETVKL 125  
137 RNVPRELEIQIEHVFVNLWYSFQDEDMFVVDLLGGLRLYHLQNVQSFEDIVRL 196  
126 FICELVNLALYQNRILHRDKPDNILLDEHGHVHTDFNIAAMLPRETOITTMATKTP 185  
197 YICEMALDYLRQSHIHRDVKPDNILLDEQGHVHTDFNIAATIKDGERATALAGTKP 256  
186 YMAPEMFSS--RKAGYSFAVDWMSLGVAYELLGRPRPHIRSTSGSKEIVHTFTTVV 243  
257 YMAPEIFHSFVNGGTGYSFVDMWMSVGMAYELLGRWRPYDIHSSNAVESLVLQFSTVS 316  
244 TYPSSANQSVSLKLLKLEPNPDQRFQSDVQVQNFPPYMDINWDVAFQKRLIFGFPNKG 303  
317 QYVPTNSKEMVALLKLLTVNPEHRSFSLQDMQAPSLAHVLDLSEKKVPEGFVFNKG 376  
304 RLNCDDPTFELEEMILESPLKHKKRIAKKEMKCDSSQT--CLLOEHLDSVQKEFII 361  
377 RLHCDPTFELEEMILESPLKHKKRIAKKNSRDSRSSQSENDYLQDCLDAIQDFVI 436  
362 FNRKVNDFNKPQNLALCTKDPQVYNGQMDGLSETFTQS 404  
437 FNRKLV-----KRSQELMSPPPGFETSDMTDSTADSEAEPTA 474

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ma A.-H.; Nelson D.A.; Xia L.; Ravi L.; Chen H.-C.; Robinson D.R.;  
RA Kung H.-J.;  
RT "PKC, A New Human AGC Group Kinase, Phosphorylates SET, a PP2A  
RT Inhibitor";  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY098866; AAM21719.1; -;  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0004688; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR002290; Ser Thr kinase.  
DR InterPro; IPR008271; Ser Thr\_pkin\_AS.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Prot kinase; 1.  
DR SMART; SM00220; S\_TKC; 1.  
DR SMART; SM00219; TyKc; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW Kinase.  
SQ SEQUENCE 486 AA; 54994 MW; 38FEFB3863B21F3 CRC64;  
Query Match 61.9%; Score 1332.5; DB 4; Length 486;  
Best Local Similarity 65.0%; Pred. No. 4.6e-100;  
Matches 233; Conservative 55; Mismatches 76; Indels 5; Gaps 3;  
QY 1 MGANTSRKPPVDEDEDVNFDFHFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKVC 60  
Db 72 MSAATARR-PVFDKEDVNFDFHFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCI 130  
QY 61 ERNEVNVKELQIMQGLEHPEFLVNLWYSFQDEDMFVVDLLGGLRLYHLQNVHFEKE 120  
Db 131 ERDEVERNPRELEIQIEHVFVNLWYSFQDEDMFVVDLLGGLRLYHLQNVQFSE 190  
QY 121 ETVKLFICELVNLALYQNRILHRDKPDNILLDEHGHVHTDFNIAAMLPRETOITTM 180  
Db 191 DTVRLTICEMALDYLRQSHIHRDVKPDNILLDEHGHVHTDFNIAATIKDGERATAL 250  
QY 181 AGTKPYMAPEMFSS--RKAGYSFAVDWMSLGVAYELLGRPRPHIRSTSGSKEIVHTF 238  
Db 251 AGTKPYMAPEIFHSFVNGGTGYSFVDMWMSVGMAYELLGRWRPYDIHSSNAVESLVL 310  
QY 239 ETTVVTYPSANQSVSLKLLKLEPNPDQRFQSDVQVQNFPPYMDINWDVAFQKRLIFG 298  
Db 311 STYSVQVPTNSKEMVALLKLLTVNPEHRSFSLQDMQAPSLAHVLDLSEKKVPEGF 370  
QY 259 IPNKGRLNCDDPTFELEEMILESPLKHKKRIAKKEMKCDSSQT--CLLOEHLDSVQ 356  
Db 371 VPNGRLHCDPTFELEEMILESPLKHKKRIAKKNSRDSRSSQSENDYLQDCLDAIQ 430  
QY 357 KEFIIIFNRKVNDFNKPQNLALCTKDPQVYNGQMDGLSETFTQS 385  
Db 431 QDFVIFNRKLVKESQDLPREPLPAPERD 459  
RESULT 11  
Q96BA3  
ID Q96BA3 PRELIMINARY; PRT; 369 AA.  
AC Q96BA3;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
TISSUE=Colon;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL; BC015792; AAH15792.1; -  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
KW Hypothetical protein; ATP-binding; Kinase;  
KW Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 369 AA; 42425 MW; 83C54CAF7D792B5 CRC64;  
Query Match 53.1%; Score 1142; DB 4; Length 369;  
Best Local Similarity 63.2%; Pred. No. 1e-84;  
Matches 216; Conservative 50; Mismatches 72; Indels 4; Gaps 2;  
QY 48 MYAMKYNKQCKVERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEDMFMVVDLLGGD 107  
DB 1 MYAMKYNKQCKIERDEVRNVFVELEILQIEHVFVNLWYSFQDEDMFMVVDLLGGD 60  
QY 108 LRVHLQNVHFKEETVKLFCELVWALDYLNQRIHRDKMKNILDEGHVHTDFNI 167  
DB 61 LRVHLQNVQFSEDTVRLYICEMALADYLRGQHIIHRDKMKNILDEGHVHTDFNI 120  
QY 168 AAMLPRETQITWAGTKPYMAPEMFSS--RKGAGYFAVDWWSLGVTAELLRRRRPYHI 225  
DB 121 ATIKOGERATAGTKPYMAPEIFHSHFVNGGTGYSEVDWWSVGVWYAYELLRGWRPYDI 180  
QY 226 RSSTSSKEIVHTFTTIVTTPSAWSQBMVSLKLLKLEPNPDQRFSQLSDVQNFYMNIDIN 285  
DB 181 HSNNAVESLQVLFSTVSQVYVPTWSKEMVALLRKLTVNPEHRLSSLDQVQAAPALAGVL 240  
QY 286 WDAVFQRLIPGFIPIKNGRLNCDPTFEEMILESKEPLHKKKKLAKKEDKMRKCDSSQT 345  
DB 241 WDHLSEKRVPEPGFVFNKGRHLCDPTFEEMILESREPLHKKKKLAKKGRDNRDSSQS 300  
QY 346 --CLLQHLDSVQKEFTIFNREKVRNDFNKPQNLALQETKD 385  
DB 301 ENDYLQCLDAIQODFVFNREKLRKRSQDLPREPLPAPESRD 342  
[1]  
SEQUENCE FROM N.A.  
TISSUE=Testis;  
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;  
RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;  
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;  
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;  
RA Datchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;  
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;

Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.;  
Rana S.S.; McQuellano N.A.; Peters G.J.; Abramson R.D.; Mullaby S.J.;  
RA Bosak S.A.; McKernan K.J.; Malek J.A.; Gumaratne P.H.;  
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;  
RA Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;  
RA Fahy J.; Helton E.; Kettaman M.; Madan A.; Rodriguez S.; Sanchez A.;  
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;  
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;  
RA Krzyzinski M.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;  
RA Jones S.J.; Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
SEQUENCE FROM N.A.  
TISSUE=Testis;  
RA Strausberg R.;  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC045760; AAH45760.1; -  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR SMART; SM00219; TyKc; 1.  
DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
SQ SEQUENCE 369 AA; 42395 MW; E152C6BB2D786B4 CRC64;  
Query Match 53.1%; Score 1142; DB 4; Length 369;  
Best Local Similarity 63.2%; Pred. No. 1e-84;  
Matches 216; Conservative 50; Mismatches 72; Indels 4; Gaps 2;  
QY 48 MYAMKYNKQCKVERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEDMFMVVDLLGGD 107  
DB 1 MYAMKYNKQCKIERDEVRNVFVELEILQIEHVFVNLWYSFQDEDMFMVVDLLGGD 60  
QY 108 LRVHLQNVHFKEETVKLFCELVWALDYLNQRIHRDKMKNILDEGHVHTDFNI 167  
DB 61 LRVHLQNVQFSEDTVRLYICEMALADYLRGQHIIHRDKMKNILDEGHVHTDFNI 120  
QY 168 AAMLPRETQITWAGTKPYMAPEMFSS--RKGAGYFAVDWWSLGVTAELLRRRRPYHI 225  
DB 121 ATIKOGERATAGTKPYMAPEIFHSHFVNGGTGYSEVDWWSVGVWYAYELLRGWRPYDI 180  
QY 226 RSSTSSKEIVHTFTTIVTTPSAWSQBMVSLKLLKLEPNPDQRFSQLSDVQNFYMNIDIN 285  
DB 181 HSNNAVESLQVLFSTVSQVYVPTWSKEMVALLRKLTVNPEHRLSSLDQVQAAPALAGVL 240  
QY 286 WDAVFQRLIPGFIPIKNGRLNCDPTFEEMILESKEPLHKKKKLAKKEDKMRKCDSSQT 345  
DB 241 WDHLSEKRVPEPGFVFNKGRHLCDPTFEEMILESREPLHKKKKLAKKGRDNRDSSQS 300  
QY 346 --CLLQHLDSVQKEFTIFNREKVRNDFNKPQNLALQETKD 385  
DB 301 ENDYLQCLDAIQODFVFNREKLRKRSQDLPREPLPAPESRD 342  
RESULT 13  
Q9BGT4 PRELIMINARY; PRT; 368 AA.  
ID Q9BGT4  
AC Q9BGT4; (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9541;

RN [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Frontal Cortex;  
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Terao K.,  
 RA Suzuki Y., Sugano S., Hashimoto K.;  
 RT "Isolation of full-length cDNA clones from macaque brain cDNA  
 RT libraries.";  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; AB056389; BAB33045.1; -;  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0016740; P:proteinase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR008271; Ser thr\_pkin\_AS.

DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Prot kinase; 1.  
 DR PROSITE; PS00011; PROTEIN KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 KW Hypothetical protein; ATP-binding; Kinase;  
 KW Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 368 AA; 42218 MW; 5D7269B32DBCC14 CRC64;

Query Match 52.4%; Score 1127.5; DB 6; Length 368;  
 Best Local Similarity 63.4%; Pred. No. 1.6e-83;  
 Matches 218; Conservative 44; Mismatches 73; Indels 9; Gaps 3;

48 MYAMKYNKQKVERNEVRNVFKELOIMQGLHHPFLVNLWYSFQDEEDMFVVDLLGGD 107  
 1 MYAMKYNKQCIERDEVRNVFRELGLQIEHFLVNLWYSFQDEEDMFVVDLLGGD 60

108 LRVHLOQNVHFKETVKLFCELYMALDYLNQRIIHRDMKPDNILLDEGHVHTDFNI 167

61 LRVHLOQNVQFSEDTVLXICEMALDYLQCGHIIHRDKVDPNILLDEGHVHTDFNI 120

168 AAMPLPRETQITMAGTYKPYAPPEFSS--RKAGYSAVDWMSLGVTAYELLGRPPYHI 225

121 ATIIKQGERATAGTKPYAPPEFSSFGVTGYSFEVDWMSLGVTAYELLGRPPYHI 180

226 RSSTSSKEIVHTFTVTVTYPSAQSQMVSLKLLLEPNPQRFSQLSDVQNFYMNIN 285

181 HSSNAVESLQVLFSTVSQVYPTWSRENVALLKLLTNPHEHFFSLQDVQAAALAGVL 240

286 WDAVFQKRLIPGFTPNKGRNLCDPTFELEEMILESKPLHKKKRLAKKEDMRKCDSSQT 345

241 WGHLSKRVPEPDFVFNKGRNLCDPTFELEEMILESKPLHKKKRLAKKEDMRKCDSSQS 300

346 --CLLQEHLSVQKEFIIFNREKYNRDPNKPQNLAEQTKDPO 387

301 ENDYLQCLDAIQDQDFVFNREKL-----KRSQDLSEPLPAPE 339

RESULT 14

ID Q21483 PRELIMINARY; PRT; 379 AA.

AC Q21483;

DT 01-NOV-1996 (TReMBLrel. 01, Created)

DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE M03C11.1 protein.

GN M03C11.1.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;

OC Rhabditidae; Pelodexinae; Caenorhabditis.

OX NCBI\_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RA McMurray A.A.;  
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA none;  
 RT "Genome sequence of the nematode C.elegans: A platform for  
 RT investigating biology.";  
 RL Science 282:2012-2018(1998).

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; Z49128; CAA88953.1; -;  
 DR PIR; T23688; T23688.  
 DR HSSP; C63450; IAO6.

DR WormPep; M03C11.1; CE03492.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0016740; P:proteinase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR002290; Ser thr\_pkinase.

DR InterPro; IPR008271; Ser thr\_pkin\_AS.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Prot kinase; 1.

DR SMART; SM00220; S\_TKc\_1.  
 DR PROSITE; PS00107; PROTEIN KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN KINASE\_DOM; 1.

DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 379 AA; 43632 MW; 5E2090A15812D27D CRC64;

Query Match 39.6%; Score 852.5; DB 5; Length 379;  
 Best Local Similarity 44.4%; Pred. No. 4e-61;  
 Matches 159; Conservative 70; Mismatches 116; Indels 13; Gaps 4;

22 HPEILRAIGKSGKGVCIQKNDTKMYAMKYNKQKVERNEVRNVFKELOIMQGLHHP 81

27 HFSVIRISGKSGKGVCIQKNTKMYAMKYNKQKVERNEVRNVFKELOIMQGLHHP 86

82 FLVNLWYSFQDEEDMFVVDLLGGDLRVHLOQNVHFKETVKLFCELYMALDYLNQRI 141

87 FLVNLWYTFQDGYMYMVSDLLGGDLRVHLSQCKGKFAEDRAKLYLCEICLAVEYLHEM 146

142 IIRDMKPDNILLDEGHVHTDFNIAMLPRETQITMAGTYKPYAPPEFSS--RKAG 199

147 IVRDKIPENILLDEGHVHTDFNIAMLPRETQITMAGTYKPYAPPEFSS--RKAG 206

200 YSAVDWMSLGVTAYELLGRPPYHIHRSSTSSKEIVHTFTVTVTYPSAQSQMVSLK 259

207 YDSRVDWMSLGVTAYELLGRPPYHIHRSSTSSKEIVHTFTVTVTYPSAQSQMVSLK 266

260 LLEPNPQRFSQLSDVQNFYMNINWDAVQKRLIPGFTPNKGRNLCDPTFELEEMILE 319

267 MLKFDKRLVGLAEIKKHSTFIDPKSVFKKPFVFPCKEGLNCDPMYLEEELV 326

320 SKPLHKKKRLAKKEDMRKCDSSQTCLQEHLSVQKEFIIFNREKYNRDPNKPQNL 377

327 STPIH--RRRTNHNSSGRSSSEFQNAALVE----VSKAFIDFSRHV-----KIEPN 373

RESULT 15

Q8WU08

ID Q8WU08 PRELIMINARY; PRT; 166 AA.

AC Q8WU08;

DT 01-MAR-2002 (TReMBLrel. 20, Created)

DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE Similar to serine threonine kinase 32.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Urinary bladder;  
RA Strausberg R.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
EMBL: BC021666; AAH21666.1; -.  
DR GO: 0005524; F:ATP binding; IEA.  
DR GO: 0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO: 0016740; F:transferase activity; IEA.  
DR GO: 0006468; F:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR008271; Ser Thr\_pkin\_AS.  
DR Pfam; PF00069; pkinase; I.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS00111; PROTEIN KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 166 AA; 19792 MW; CDCF94E54C793BA4 CRC64;

Query Match 38.8%; Score 835; DB 4; Length 166;  
Ident Local Similarity 100.0%; Pred. No. 3.6e-60;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGKVCIVQKNDTKKMYAMKYNKQCV 60  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGKVCIVQKNDTKKMYAMKYNKQCV 60  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFE 120  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFE 120  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 121 ETVKLFICELVMDYLDYLNQRIIHRDMKPNILLDEH 157  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 121 ETVKLFICELVMDYLDYLNQRIIHRDMKPNILLDEH 157  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Search completed: May 26, 2004, 20:19:48  
Job Name : 47 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 26, 2004, 20:09:03 ; Search time 18 Seconds  
(without alignments)  
1177.364 Million cell updates/sec

Title: US-10-620-845-9  
Perfect score: 2151  
Sequence: 1 MGNTSRKPPVDFEDNDF.....VTNGQMDTGLSETPQTSKVS 407

Search table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Sequences: 141681 seqs, 52070155 residues  
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	DB	ID	Description
1	595.5	27.7	444	1	KRAC_DICDI	P54644 dictyosteli
2	546	25.4	479	1	PK2_DICDI	P28178 dictyosteli
3	537.5	25.0	648	1	KAPC_DICDI	P34099 dictyosteli
4	532	24.7	471	1	KP19_ARATH	P39030 arabidopsis
5	529.5	24.6	465	1	KPK1_ARATH	P42818 arabidopsis
6	526	24.6	680	1	YPK1_YEAST	P12688 saccharomyc
7	521.5	24.2	352	1	KAPC_DROME	P12370 drosophila
8	519.5	24.2	696	1	SKK1_SCHPO	P50530 schizosacch
9	514.5	23.9	740	1	K6A3_HUMAN	P51812 homo sapien
10	514.5	23.9	740	1	K6A3_MOUSE	P18654 mus musculu
11	514.5	23.9	823	1	SCB3_YEAST	P11792 saccharomyc
12	514	23.9	404	1	KAPC_CAEEL	P21137 caenorhabdi
13	514	23.9	677	1	YPK2_YEAST	P18961 saccharomyc
14	513.5	23.9	350	1	KAPA_CRIGR	P25321 cricetulus
15	513.5	23.9	733	1	K6A2_HUMAN	Q15349 homo sapien
16	511.5	23.8	350	1	KAPG_HUMAN	P22612 homo sapien
17	509.5	23.7	350	1	KAPA_HUMAN	P17612 homo sapien
18	509.5	23.7	350	1	KAPA_PIG	P36887 sus scrofa
19	509.5	23.7	350	1	KAPA_RAT	P27791 rattus norv
20	509.5	23.7	350	1	KAPA_SHEEP	Q9mzd9 ovis aries
21	509.5	23.7	733	1	K6A2_MOUSE	Q9wtu3 m ribosomal
22	508.5	23.6	586	1	KPCI_MOUSE	Q62074 mus musculu
23	508.5	23.6	587	1	KPCI_HUMAN	P41743 homo sapien
24	507.5	23.6	350	1	KAPA_BOVIN	P00517 bos taurus
25	507.5	23.6	752	1	K6AA_CHICK	P18652 gallus gall
26	507	23.6	350	1	KAPB_MOUSE	P05206 mus musculu
27	505	23.5	646	1	KDBE_SCHPO	Q10364 schizosacch
28	505.5	23.5	349	1	KAPA_CANFA	Q8mj44 canis fami
29	504.5	23.5	398	1	KAPC_YEAST	P05986 saccharomyc
30	504.5	23.5	733	1	K6AA_XENLA	P10665 xenopus lac
31	503.5	23.4	350	1	KAPA_MOUSE	P05132 mus musculu
32	503.5	23.4	689	1	ARK1_HUMAN	P25098 homo sapien
33	501.5	23.3	629	1	K6AB_XENLA	P10666 xenopus lac

RESULT 1  
KRAC\_DICDI  
ID KRAC\_DICDI STANDARD; PRT; 444 AA.  
AC P54644;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE RAC-family serine/threonine kinase homolog (EC 2.7.1.-).  
GN PKGA OR DAGA.  
OS Dictyostelium discoideum (slime mold).  
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
OX NCBI\_TaxID=44689;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AX3;  
RA Moon B., Haribabu B., Rabino M., Ortiz B., Reichel G., Shehel P.,  
RA Williams J., Bouzid S., Veron M., Dotti R.P.;  
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. RAC  
CC SUBFAMILY. STRONGEST TO YEAST YPK1/YPK2.  
CC -!- SIMILARITY: Contains 1 PH domain.

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-----  
EMBL: U15210; AAA76692.1; --  
RSP; P05132; ICTP.  
DictyBase; DDB0003794; pkba.  
InterPro; IPR001849; PH.  
InterPro; IPR000961; Pkinase C.  
InterPro; IPR000719; Prot kinase.  
InterPro; IPR008271; Ser thr pkin AS.  
InterPro; IPR002230; Ser\_thr\_kinase.  
Pfam; PF00169; PH; 1.  
Pfam; PF00069; pkinase; 1.  
Pfam; PF00433; pkinase C; 1.  
ProDom; PD000001; Prot\_kinase; 1.  
SMART; SM00233; PH; 1.  
SMART; SM00133; S\_TK\_X; 1.  
SMART; SM00220; S\_TK\_X; 1.  
PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
PROSITE; PS00108; PROTEIN KINASE ST; 1.  
PROSITE; PS00111; PROTEIN KINASE DW; 1.  
PROSITE; PS00003; PH DOMAIN; 1.  
Transferase; Serine/threonine-protein kinase; ATP-binding.  
DOMAIN 5 100 PH.  
FT NP BIND 120 374 ATP (BY SIMILARITY).  
FT BINDING 126 134 ATP (BY SIMILARITY).  
FT ACT SITE 149 149 ATP (BY SIMILARITY).  
FT ACT SITE 243 243 BY SIMILARITY.  
SEQUENCE 444 AA; 51062 MW; 12367AJA411C5680 CRC64;

34 501 23.3 512 1 KAPB\_SCHPO  
35 500.5 23.3 745 1 K6A6\_HUMAN  
36 498.5 23.2 479 1 AKT3\_HUMAN  
37 498.5 23.2 479 1 AKT3\_MOUSE  
38 498.5 23.2 689 1 ARK1\_BOVIN  
39 498 23.2 380 1 KAPB\_YEAST  
40 498 23.2 689 1 ARK1\_MESAU  
41 497.5 23.1 350 1 KAPB\_HUMAN  
42 497.5 23.1 689 1 AKK1\_RAT  
43 497.5 23.1 735 1 K6A1\_HUMAN  
44 497 23.1 350 1 KAPB\_BOVIN  
45 497 23.1 397 1 KAPI\_BOVIN

ALIGNMENTS

Sequence: 1 MGNTSRKPPVDFEDNDF.....VTNGQMDTGLSETPQTSKVS 407

Search table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Sequences: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	DB	ID	Description
1	595.5	27.7	444	1	KRAC_DICDI	P54644 dictyosteli
2	546	25.4	479	1	PK2_DICDI	P28178 dictyosteli
3	537.5	25.0	648	1	KAPC_DICDI	P34099 dictyosteli
4	532	24.7	471	1	KP19_ARATH	P39030 arabidopsis
5	529.5	24.6	465	1	KPK1_ARATH	P42818 arabidopsis
6	526	24.6	680	1	YPK1_YEAST	P12688 saccharomyc
7	521.5	24.2	352	1	KAPC_DROME	P12370 drosophila
8	519.5	24.2	696	1	SKK1_SCHPO	P50530 schizosacch
9	514.5	23.9	740	1	K6A3_HUMAN	P51812 homo sapien
10	514.5	23.9	740	1	K6A3_MOUSE	P18654 mus musculu
11	514.5	23.9	823	1	SCB3_YEAST	P11792 saccharomyc
12	514	23.9	404	1	KAPC_CAEEL	P21137 caenorhabdi
13	514	23.9	677	1	YPK2_YEAST	P18961 saccharomyc
14	513.5	23.9	350	1	KAPA_CRIGR	P25321 cricetulus
15	513.5	23.9	733	1	K6A2_HUMAN	Q15349 homo sapien
16	511.5	23.8	350	1	KAPG_HUMAN	P22612 homo sapien
17	509.5	23.7	350	1	KAPA_HUMAN	P17612 homo sapien
18	509.5	23.7	350	1	KAPA_PIG	P36887 sus scrofa
19	509.5	23.7	350	1	KAPA_RAT	P27791 rattus norv
20	509.5	23.7	350	1	KAPA_SHEEP	Q9mzd9 ovis aries
21	509.5	23.7	733	1	K6A2_MOUSE	Q9wtu3 m ribosomal
22	508.5	23.6	586	1	KPCI_MOUSE	Q62074 mus musculu
23	508.5	23.6	587	1	KPCI_HUMAN	P41743 homo sapien
24	507.5	23.6	350	1	KAPA_BOVIN	P00517 bos taurus
25	507.5	23.6	752	1	K6AA_CHICK	P18652 gallus gall
26	507	23.6	350	1	KAPB_MOUSE	P05206 mus musculu
27	505	23.5	646	1	KDBE_SCHPO	Q10364 schizosacch
28	505.5	23.5	349	1	KAPA_CANFA	Q8mj44 canis fami
29	504.5	23.5	398	1	KAPC_YEAST	P05986 saccharomyc
30	504.5	23.5	733	1	K6AA_XENLA	P10665 xenopus lac
31	503.5	23.4	350	1	KAPA_MOUSE	P05132 mus musculu
32	503.5	23.4	689	1	ARK1_HUMAN	P25098 homo sapien
33	501.5	23.3	629	1	K6AB_XENLA	P10666 xenopus lac



Query Match 27.7%; Score 595.5; DB 1; Length 444;  
 Best Local Similarity 38.9%; Pred. No. 6.9e-33;  
 Matches 122; Conservative 69; Mismatches 108; Indels 15; Gaps 6;

QY 4 NTSRKPVPDENEDVDFEILRAIGKSGFVCIVQKNDTKKMYAMKQKCVERN 63  
 DB 104 NGKQP---KSKGVADPELNLVKGSGFGVIQVRKDTGEVYAMKVLKSHIVEIN 160

QY 64 EYENVEKLEIQMGLGHPFLVNLWYFQDEEDMFVVDLLGGDLRYHLQONVHFKEETV 123  
 DB 161 EYEHTLSERNILQKINHPFLVNLWYFQDEEDMFVVDLLGGDLRYHLQONVHFKEETV 220

QY 124 KLFICELVALDYLNQRIHRDMKPDNILLDEHGHVHTDFNIA--AMLPRETQITTTWA 181  
 DB 221 RYTGAEIVALEHLHLSGVIYRDLKPEKLNLLTNEGHICMTDFGLCKEGLLTPTDKGTFC 280

QY 182 GTKPYMAPEMFSSRKAGYSFAVDWMSLGVATYELLGRPRPVHRSSTSSKSEVHTFTT 241  
 DB 281 GIPEYLAPEVL---QNGVGKQVDWMSFGLLYEMLTGLPPFY---NQDVQMYRKIMME 334

QY 242 VVTYPSAWQEMVSLKLLEPNPDQRFSQLSDVQNFPPYMNIDINWDAVFQKRLIPGFIPN 301  
 DB 335 KLSFPHFISPDARSLLQLERDPKRLADPNLKRHPFRSIDWQLFKQKIPPPFIEN 394

QY 302 -KGRLN---CDPTF 311  
 DB 395 VRGSADTSQIDPVF 408

RESULT 2  
 PK2\_DICDI STANDARD; PRT; 479 AA.  
 AC P28178;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DB Protein kinase 2 (EC 2.7.1.-).  
 GN PKGB OR PFKA.  
 OS Dictyostelium discoideum (Slime mold).  
 CC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
 CC NCBI\_TaxID=44689;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC MEDLINE=91142122; PubMed=1996312;  
 CC Haribabu B., Dotti R.P.;  
 CC "Identification of a protein kinase multigene family of Dictyostelium  
 CC discoideum: molecular cloning and expression of a cDNA encoding a  
 CC developmentally regulated protein kinase.";  
 CC Proc. Natl. Acad. Sci. U.S.A. 88:1115-1119(1991).  
 CC -!- DEVELOPMENTAL STAGE: KINASE 2 ENCODES A 2.0 KB AND A 2.2 KB  
 CC TRANSCRIPT. THE SMALLER ONE IS EXPRESSED IN VEGETATIVE CELLS, AND  
 CC THE LARGER ONE DURING DEVELOPMENT.  
 CC -!- INDUCTION: The 2.2 kb transcript is probably induced by exogenous  
 CC CAMP via a cell-surface receptor-mediated signal transduction  
 CC pathway.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. S6  
 CC kinase subfamily.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M59744; AAA33186.1; -;  
 CC FIR; A38578; A38578.  
 CC HSSP; P05132; 1CTP.  
 CC DictyBase; DDB0002054; pkGB.  
 CC InterPro; IPR000961; kinase C.  
 CC InterPro; IPR000719; Prot\_kinase.

DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; kinase; 1.  
 DR Pfam; PF00433; kinase C; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00220; S\_TK; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 KW Transferase; Serine/threonine-protein kinase; ATP-binding; CAMP;  
 KW Phosphorylation.  
 FT DOMAIN 53 60 POLY-GLN.  
 FT DOMAIN 73 77 POLY-GLN.  
 FT DOMAIN 153 407 PROTEIN\_KINASE.  
 FT NP\_BIND 159 167 ATP (BY SIMILARITY).  
 FT BINDING 182 182 ATP (BY SIMILARITY).  
 FT ACT\_SITE 276 276 BY SIMILARITY.  
 FT MOD\_RES 309 309 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 SQ SEQUENCE 479 AA; 52963 MW; E0015C08E397105 CRC64;

Query Match 25.4%; Score 546; DB 1; Length 479;  
 Best Local Similarity 36.5%; Pred. No. 1.5e-29;  
 Matches 118; Conservative 66; Mismatches 123; Indels 16; Gaps 6;

QY 11 VFDEN-EDVNFDFEILRAIGKSGFVCIVQKNDTKKMYAMKQKCVERNVNF 69  
 DB 143 IFSKNQKQATKDDFELLNVIGKSGFQVQVKKGEDKIFAMKVLKDAIARKQVNHTK 199

QY 73 KLEQIMQGLEHPPFLVNLWYFQDEEDMFVVDLLGGDLRYHLQONVHFKEETVKLFICE 129  
 DB 203 SEKTILQICSHFPFLVNLWYFQDEEDMFVVDLLGGDLRYHLQONVHFKEETVKLFICE 259

QY 133 LYVALDYLNQRIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETQITTMAGTKPYMAP 189  
 DB 263 IVSALDHLKQDIVYRDLKPEKLNLLTNEGHICMTDFGLCKEGLLTPTDKGTFC 319

QY 193 EMFSSRKAGYSFAVDWMSLGVATYELLGRPRPVHRSSTSSKSEIVHTFTTVPYPSAW 249  
 DB 323 EVLN---GHGHCVAVDWMSLGLTYEMLTGLPPFYQNVSTWYQKILNGELXIPY---I 373

QY 253 SOEYSLKLLEPNPDQRFSQL---SDVQNFPPYMNIDINWDAVFQKRLIPGFIP---NKG 303  
 DB 374 SPEAKSLLEGLLTRVDKRLGTGKGGEVQKHPFKNIDWEKLDKREVEVHFAPKVKSGTD 433

QY 304 RUNCDDPTFELE---EMILESKEPL 323  
 DB 434 ISQIDPVFTQERPMDSLVETSAL 456

RESULT 3  
 ID KAPC\_DICDI STANDARD; PRT; 648 AA.  
 AC P34039;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE CAMP-dependent protein kinase catalytic subunit (EC 2.7.1.37).  
 GN PKAC OR PK2 OR PK3.  
 OS Dictyostelium discoideum (Slime mold).  
 CC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
 CC NCBI\_TaxID=44689;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC MEDLINE=91323730; PubMed=1864510;  
 CC Buerki Z., Anjard C., Scholder J.-C., Raymond C.D.;  
 CC "Isolation of two genes encoding putative protein kinases regulated  
 CC during Dictyostelium discoideum development.";  
 CC Gene 102:57-65(1991).  
 CC [2]  
 CC CHARACTERIZATION.

RX MEDLINE=93385090; PubMed=8373760;  
 RA Anjard C., Ecchebehere L., Pinaud S., Veron M., Raymond C.D.;  
 RT "An unusual catalytic subunit for the CAMP-dependent protein kinase  
 of Dictyostelium discoideum.";  
 RL Biochemistry 32:9532-9538(1993).  
 RN [3]  
 RP CHARACTERIZATION.  
 RC STRAIN=AX3; PubMed=1332055;  
 RX Mann S.K.O., Yonemoto W.M., Taylor S.S., Firtel R.A.;  
 RA "dapK3, which plays essential roles during Dictyostelium development,  
 encodes the catalytic subunit of CAMP-dependent protein kinase.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:10701-10705(1992).  
 CC - FUNCTION: Essential for differentiation and fruit morphogenesis.  
 CC - CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC - SUBUNIT: IN DICTYOSTELIUM THE Holoenzyme is a dimer COMPOSED OF  
 A REGULATORY (R) AND A CATALYTIC (C) SUBUNIT. IN THE PRESENCE OF  
 CAMP IT DISSOCIATES INTO THE ACTIVE C SUBUNIT AND AN R MONOMER.  
 CC - DEVELOPMENTAL STAGE: CAPK activity is low in vegetatively growing  
 amoebae, increases during development of aggregation and reaches  
 a maximum at culmination.  
 CC - SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CAMP  
 subfamily.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; M38703; -; NOT ANNOTATED\_CDS.  
 CC PIR; JQ1150; JQ1150.  
 CC HSP; P05132; IATP.  
 CC DictyBase; DDB0003793; pkac.  
 CC InterPro; IPR000961; protein kinase C.  
 CC InterPro; IPR000719; prot\_kinase.  
 CC InterPro; IPR008271; Ser\_thr\_kinase.  
 CC InterPro; IPR002290; Ser\_thr\_kinase.  
 CC InterPro; IPR001245; Tyr\_kinase.  
 CC Pfam; PF00069; pkinase; 1.  
 CC Pfam; PF00433; pkinase C; 1.  
 CC PRINTS; PR00109; TYRKINASE.  
 CC ProDom; PD000001; Prot\_kinase; 1.  
 CC SMART; SM00133; S\_TK\_X; 1.  
 CC SMART; SM00220; S\_TK; 1.  
 CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 CC PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 CC PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
 CC Transferase; Serine/threonine-protein kinase; ATP-binding; CAMP;  
 KW Phosphorylation.  
 FT DOMAIN 58 64 ASN-RICH.  
 FT DOMAIN 136 223 GLN-RICH.  
 FT DOMAIN 233 250 THR-RICH.  
 FT DOMAIN 336 590 PROTEIN KINASE.  
 FT NP\_BIND 342 350 ATP (BY SIMILARITY).  
 FT BINDING 365 365 ATP (BY SIMILARITY).  
 FT ACT\_SITE 459 459 BY SIMILARITY.  
 FT MOD\_RES 490 490 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 648 AA; 74458 MW; D0F9B3A48C58D084 CRC64;  
 Query Match 25.08; Score 537.5; DB 1; Length 648;  
 Best Local Similarity 34.18; Pred. No. 8.2e-29;  
 Matches 109; Conservative 74; Mismatches 120; Indels 17; Gaps 6;  
 QY 9 PPVDEEDNVDFHLLRAIGKSGFKVCIVQKNDTKQYAMKYNKQKCVNEVNV 68  
 DB 325 PPV---NARELKEFKQIRVLGTGTGKVLQNTKDGCVYAMKLNKAVVQLKQVEHL 381  
 QY 69 FKEIQIMQGLEHPLVNLWTSFQDEDMFVMDLLGLGDLRYHLQNVHFKETVKLFIC 128  
 DB 382 NSEKILLSIHPPVNLVYQAFQDEKLLYLLFYVAGGEVTHLRKSMKFSNSTAKFYAA 441

QY 129 ELVWALDYLNQRIIHRDMKPNILLDEGHVHTDNIAMLPRETQITTMAGTKPYMA 188  
 DB 442 EIVLALFLHKNIVYRDLKPNLLDQNGHIIKTDGFAKRV--EDRTTLCGTPPYLA 499  
 QY 189 PEMFSRKGAGYSFVNDWSLGVTAVELLRGRPYHRSSTSSKEIVHTFTTVPYPSA 248  
 DB 500 PEIIQSK---GHGKAVDWNALGILIFEMLAGYPPFY---DDDTFAIYNKILAGRIITPLG 553  
 QY 249 WSOEMVSLKLLKLEPNPDQRFSQLS-----DVQNPYPYNDINWDAVQKRLIPGIPNKGR 304  
 DB 554 FDVDAKDLIKELLTADRTRRLGALKDGLAVDQVHRWFSNDINWERYLQRRDNGPPFIPKIQH 613  
 QY 305 LNCDDPTFEL--EMILESXP 322  
 DB 614 QGDSSNFEMYEDEEMVEPP 633  
 RESULT 4  
 KP19 ARATH STANDARD; PRT; 471 AA.  
 AC Q33030; Q949X5; Q9C5R1;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Serine/threonine-protein kinase AtPK19 (EC 2.7.1.1-) (Ribosomal-protein  
 S6 kinase homolog).  
 GN ATPK19 OR AT3G08720 OR F17014.19.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=95129712; PubMed=7828736;  
 RA Mizoguchi T., Hayashida N., Yamaguchi-Shinozaki K., Kamada H.,  
 RA Shinozaki K.;  
 RT "Two genes that encode ribosomal-protein S6 kinase homologs are  
 induced by cold or salinity stress in Arabidopsis thaliana.";  
 RL FEBS Lett. 358:199-204(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=21016720; PubMed=11130713;  
 RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseid M.,  
 RA Partman B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,  
 RA Delbeny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,  
 RA De Simone V., Choisine N., Artiguenave F., Robert C., Brottier P.,  
 RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quettier F.,  
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,  
 RA Wurmbach E., Drzonek H., Erle H., Jordan N., Bangert S.,  
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,  
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simionati B.,  
 RA Conrad A., Hornischer K., Kauer G., Loebner T.-H., Nordstiek G.,  
 RA Reichelt J., Scharfe M., Schoen O., Barges M., Terol J., Climent J.,  
 RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,  
 RA Cooke R., Laudie M., Berger-Lilauro C., Purnelle B., Masuy D.,  
 RA De Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,  
 RA Monfort A., Agirrou A., Flores M., Liguori R., Vitale D.,  
 RA Mannhaupt G., Haase D., Schoof H., Rued S., Zaccaria P., Mewes H.-W.,  
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,  
 RA Rooney T., Rizzo M., Waits A., Utterback T., Fujii C.Y., Shen T.P.,  
 RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,  
 RA Pai G., Miltscher J., Sellers P., Gill J.E., Feldblum T.V.,  
 RA Praus D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,  
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asanizu E.,  
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,  
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
 RA Watanabe A., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,  
 RA Watanabe S., Yamada M., Yasuda M., Tabata S.;  
 RT "Sequencing and analysis of chromosome 3 of the plant Arabidopsis

thaliana.";

[3]

SEQUENCE FROM N.A.

STRAIN=cv. Columbia;

Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,

Palm C.J., Theologis A., Ecker J., Davis R.W.;

Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

[4]

SEQUENCE FROM N.A.

STRAIN=cv. Columbia;

MEDLINE=22954850; PubMed=14593172;

Yamada K., Lim J.M., Dale J.M., Chen H., Shinn P., Palm C.J.,

Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

Karlin-Neumann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

Miranda M., Quach H.L., Tripp M., Chang J.M., Lee J.M., Toriumi M.J.,

Chan M.M., Tang C.C., Onodera C.S., Deng J.H., Akiyama K., Ansari Y.,

Arakawa T., Bann J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,

Khan S., Koeseema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

Satou M., Tanse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,

Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Empirical analysis of transcriptional activity in the Arabidopsis

genome.";

Science 302:842-846(2003).

CC -!- FUNCTION: May be involved in adaptation of plant to cold or high-

CC salt conditions.

CC -!- PTM: Undergoes serine-specific autophosphorylation (By

CC similarity).

CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. S6

CC kinase subfamily.

CC -!- CAUTION: Ref. 4 sequence differs from that shown due to a

CC frameshift in position 391.

-----

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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

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EMBL; D42061; BRA07661.1; -;

EMBL; AC012562; AAG51345.1; -;

EMBL; AF325094; AAK17162.1; -;

EMBL; AY050826; -; NOT\_ANNOTATED\_CDS.

PIR; S68463; S68463.

HSSP; P05132; ICRP.

InterPro; IPR000961; Pkinase\_C.

InterPro; IPR000719; Prot Kinase.

InterPro; IPR008271; Ser\_thr\_pkin\_AS.

InterPro; IPR002290; Ser\_thr\_pkinase.

Pfam; PF00069; pkinase; 1.

Pfam; PF00433; pkinase\_C; 1.

ProDom; PD000001; Prot Kinase; 1.

SMART; SM00133; S TK X; 1.

SMART; SM00220; S TKG; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.

PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.

Transferrase; Serine/threonine-protein kinase; ATP-binding;

Phosphorylation.

DOMAIN 140 395 PROTEIN KINASE.

FT NP BIND 146 154 ATP (BY SIMILARITY).

FT BINDING 169 199 ATP (BY SIMILARITY).

FT ACT SITE 263 263 BY SIMILARITY.

FT CONFLICT 250 250 A -> V (IN REF. 1).

FT CONFLICT 359 360 LS -> VF (IN REF. 1).

SEQUENCE 471 AA; 53037 MW; 95F007B44B58DFB5 CRC64;

Query Match

24.7%; Score 532; DB 1; Length 471;

Best Local Similarity 34.6%; Pred No. 1.3e-28;

Matches 110; Conservative 63; Mismatches 121; Indels 24; Gaps 4;

QY 12 FDENED-----VNFDFEILRAIGKSGFKYCIYQKNDTKMYAMYNKOK 58

DB 116 FSGNDTDSKSPSEVSGVVGIEDFEVLKVGQGAFGKYQVRKDTSEIYAMKVRKDK 175

QY 59 CYVERNEVRNVFELQIMQGLEHPLVNLWYSQDEEDMEFVVDLLGGDLRYHLQNVHF 118

DB 176 IVEKNHAEYMKAEERDILTKIDHPFVQLKYSFQTKRYLYLVLDINGGHLFQLYHQGLF 235

QY 119 KEETVKLFCELVMDYIQNORIIHRDMKPNILIDEGHVHIITDFNIAAMLPRETOIT 178

DB 236 REDLARVYTAETVSASHLHEKIMERDLKPNILMDVGHVWLTDFGLAKEFEETRNS 295

QY 179 TWAGTKPYMAPEMFSSKAGYSAFVDMWSLGVYAVELLGRRRPYHIRSTSKSEIVHTF 238

DB 296 SMCGTTEYMAPEIV--RGKHDKAADWNSVGLLYMLTKGPPFLGSGKIQOKIV-- 349

QY 239 EYTVVTPYSAWQSEMYSLAKLLEPNDFQF-----SOLSDVQNFPMYNDINNDVAFQKL 294

DB 350 -KDKIKLPOLFSNEAHALLKGLLQKEPERRLGSGPSGAEEIKHKWFKALNWKLEAREV 408

QY 295 IPGFIPNKGRLNCDPTFE 312

DB 409 QPSFKPAVSGRQCIANFD 426

RESULT 5

ID\_KPK1\_ARATH STANDARD; PRT; 465 AA.

AC P42818;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Serine/threonine-protein kinase AtPK1/AtPK6 (EC 2.7.1.1-).

GN ATPK1 OR ATPK6 OR AT3G08730 OR F17014.20.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.

OC NCBI\_TaxID=3702;

CX [1]

RN SEQUENCE FROM N.A.

RP STRAIN=cv. Landsberg erecta;

RX MEDLINE=94292519; PubMed=7912697;

RA Zhang S.-H., Lawton M.A., Hunter T., Lamb C.J.;

RT "AtPK1, a novel ribosomal protein kinase gene from Arabidopsis. I.

RT Isolation, characterization, and expression.";

RL J. Biol. Chem. 269:17586-17592(1994).

RL [2]

RN SEQUENCE FROM N.A.

RP STRAIN=cv. Columbia;

RX MEDLINE=95129712; PubMed=7828736;

RA Mizoguchi T., Hayashida N., Yamaguchi-Shinozaki K., Kamada H.,

RA Shinozaki K.;

RT Two genes that encode ribosomal-protein S6 kinase homologs are

RT induced by cold or salinity stress in Arabidopsis thaliana.";

RL FEBS Lett. 358:199-204(1995).

RL [3]

RN SEQUENCE FROM N.A.

RP STRAIN=cv. Columbia;

RX MEDLINE=21016720; PubMed=11130713;

RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unseld M.,

RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,

RA Deleney M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,

RA De Simone V., Choisme N., Artiguenave F., Robert C., Brottier P.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,

RA Wurmbach E., Drzonek H., Brfle H., Jordan N., Bangert S.,

RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,

RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,

RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,

RA Reichelt J., Scharfe M., Schoen O., Barques M., Terol J., Climent J.,  
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,  
RA Cooke R., Laidie M., Berger-Liauro C., Purnelle B., Masuy D.,  
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,  
RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,  
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,  
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,  
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,  
RA Greasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,  
RA Pai G., Millican J., Sellers P., Gill J.E., Felsblyum T.V.,  
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,  
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,  
RA Sasamoto S., Kimura T., Idegawa K., Kawashima K., Kishida Y.,  
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
RA Nakayama S., Nakazaki N., Shindo S., Takeuchi C., Wada T.,  
RA Watanabe A., Yamada M., Yasuda M., Tabata S.,  
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis  
RL thaliana.";  
RL Nature 408:820-822(2000).  
RN [4]  
RN CHARACTERIZATION.  
RN STRAIN=cv. Landsberg erecta;  
RX MEDLINE=94292520; PubMed=8021267;  
RA Zhang S.-H., Broome M.A., Lawton M.A., Hunter T., Lamb C.J.;  
RT "AtpK1, a novel ribosomal protein kinase gene from Arabidopsis. II.  
RT Functional and biochemical analysis of the encoded protein.";  
RN J. Biol. Chem. 269:17593-17599(1994).  
CC -!- FUNCTION: Could be involved in the control of plant growth and  
CC development. Phosphorylates two ribosomal proteins, P14 and P16.  
CC -!- TISSUE SPECIFICITY: Expressed in all tissues.  
CC -!- DEVELOPMENTAL STAGE: Predominates during high metabolic activity  
CC in growing buds, root tips, leaf margins and germinating seeds.  
CC -!- PTM: Undergoes serine-specific autophosphorylation.  
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. S6  
CC kinase subfamily.  
CC  
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
DR EMBL; L29030; AAA21142.1; -;  
DR EMBL; D42056; BAA07656.1; -;  
DR EMBL; AC012562; AAG51351.1; -;  
DR PIR; S68462; S68462.  
DR InterPro; IPR000961; Pkinase C.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR Pfam; PF00069; pkinase; 1.  
DR Pfam; PF00433; pkinase C; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TK; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.  
KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
KW phosphorylation.  
FT DOMAIN 134 389 PROTEIN KINASE.  
FT NP BIND 140 148 ATP (BY SIMILARITY).  
FT BINDING 163 163 ATP (BY SIMILARITY).  
FT ACT SITE 257 257 BY SIMILARITY.  
FT MUTAGEN 163 163 K-R: ACTIVITY SUBSTANTIALLY DIMINISHED.  
SQ SEQUENCE 465 AA; 5258 MW; 407133D674CA271F CRC64;  
Query Match 24.6%; Score 529.5; DB 1; Length 465;  
Best Local Similarity 34.8%; Pred. No. 1.9e-28;  
Matches 104; Conservative 65; Mismatches 119; Indels 11; Gaps 3;

QY 18 VNFDFHILRAIGKSGKVCIVQNDTKMAYKYNKQKCVERNVNFVKELQIQMG 77  
DB 129 VGIDDFEVMKVVKGAFKVVQVRKETSIIYAMKWKQKHIMEKNHAYMKAEIDIITK 188  
QY 78 LEHFLYLNWYSFODEEDMFVWVLLAGGLRYHLQNVHFKETVKLIFICELYMALDYL 137  
DB 189 IDHFFIIVQLKYSFQTKRYLVLDVDFINGHLFFQYHQGLFREDLARVYTAIYSAVSHL 248  
QY 138 QNQRHIIHRDKMPDNILLDEHGHVHTDFTNIAAMLPRETOITTMAGTKPYMAPEMPSSKRG 197  
DB 245 HEKIMRDLKXENILMDTGHVMTLDTFLAKFEENRSMCGTTEYMAPEIV--RG 305  
QY 195 AGYSFAVDMWSLGVATVYELLGRGPPYHIRSTSKSKEIVHIFETTVVYPSAWSQEMVSL 257  
DB 305 KGHDKAADWMSVGILLYEMLTGKPPFLGSGKGIQOKIV---KDKIKLPQFLSNEAHAIL 361  
QY 255 KLLLEPNPDQR----FSQLSDVQNFPPYNDINWDVQKRLIPGIPNKGRLNCDPTE 312  
DB 362 KGLLQKEPERRLGSLGAAEIKQHKWFKGINWKKLEAREVNPSEKPEVSGRQCIANED 420

## RESULT 6

YPK1 YEAST  
ID YPK1 YEAST STANDARD; PRT; 680 AA.  
AC P12688;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Serine/threonine-protein kinase YPK1 (EC 2.7.1.-).  
GN YPK1 OR YKL126W.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89090805; PubMed=2850145;  
RA Maurer R.A.;  
RT "Isolation of a yeast protein kinase gene by screening with a  
RT mammalian protein kinase cDNA.";  
RL DNA 7:459-474(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Rad M.R., Xu G., Kirchrath L., Fritz C., Keuchel H., Hollenberg C.P.;  
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP DISCUSSION OF SEQUENCE.  
RX MEDLINE=93173125; PubMed=8437590;  
RA Chen P.-C., Lee K.S., Levin D.E.;  
RT "A pair of putative protein kinase genes (YPK1 and YPK2) is required  
RT for cell growth in Saccharomyces cerevisiae.";  
RL Mol. Gen. Genet. 236:443-447(1993).  
CC -!- FUNCTION: Plays an essential role in the proliferation of yeast  
CC cells.  
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC RAC SUBFAMILY. STRONGEST TO YPK2.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; M21307; AAA34880.1; -;  
DR EMBL; 228126; CAA81967.1; -;  
DR PIR; S37955; S37955.  
DR HSP; F05132; 1CTP.  
DR GenOnline; 139882; -;  
DR SGD; SC001609; YPK1.  
DR GO; GO:0005935; C:bud neck; IDA.

```
DR GO: GO:0005829; Cytosol; IDA.
DR GO: GO:0005886; C:plasma membrane; IDA.
DR GO: GO:0004674; P:protein serine/threonine kinase activity; IMP.
DR GO: GO:0006897; P:endocytosis; IMP.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IMP.
DR GO: GO:0006665; P:sphingolipid metabolism; IMP.
DR InterPro: IPR000961; Pkinase.C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; I.
DR Pfam: PF00433; pkinase.C; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00133; S TK X; 1.
DR SMART: SM00220; S TK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR TRANSFASER: Serine/threonine-protein kinase; ATP-binding.
DOMAIN 347 602 PROTEIN_KINASE.
NP_BIND 353 361 ATP (BY SIMILARITY).
BINDING 376 376 ATP (BY SIMILARITY).
ACT_SITE 470 470 BY SIMILARITY.
CONFLICT 201 201 P -> L (IN REF. 2).
CONFLICT 553 553 M -> I (IN REF. 2).
SEQUENCE 680 AA; 76479 MW; 00112BBB849CD2B5 CRC64;
Query Match 24.5%; Score 526; DB 1; Length 680;
Query Local Similarity 32.6%; Pred. No. 5,1e-28;
Matches 117; Conservative 77; Mismatches 123; Indels 42; Gaps 10;
8 KPPVDEEDVNFHFEILRAIGKSGFKVCIQVQNDTKKMYKMKQKCVNEVRN 67
335 KP--SRNKSIDFDLLKVIKSGFKQVQRKDKTKVYALKAIKRSIVYKSEVTH 391
68 VFKEIQVQGLEHPEPLVNLWSFQDEDMVWVLLGLGLRYHLQNVHKEETVKLF 127
392 TLAEKTVLARDVCPVLEPKFSQPEKLYFVLAFINGGELFYHLQKGRFDLSAREY 451
128 CELVMDYLQVRIHDMKPDNILLDEHGHVHTDFENIAAMLPRETQIT--TWAGTRPY 186
452 AELLCALDNLHLKDVYRDLKPEINLLOYQGHIALCDGLCKLNKMDKDKDTFCGTPEY 511
187 MAPEMFSRKGAGYFAVDWWSLGVATVELLGRPPYHIRSTSKSEIVHTFTV--V 243
512 LAPELL---LGLGYTKAVDWTGLVLLYEMLTGLPPY-----DEDVPMYKKILQEP 562
244 TYPSSAWSEWVSLKLLKLEPNPQDQ--FSQLSDVQNFPMNDINWDVQKRLIPGTPN 301
563 VPDGFDKADKDLGLLSRDPTRRLGLNGDAEIRNHEFFQLSKWRLMKGYIPPYKPA 622
302 KGRNLCDPTFELEEMILESPLHKKKRLAKKEDMRKCDSSQTCLLQEH--DSVQKEF 359
623 VS--NSMDTSNFDREFTREKPI-----DS-----VVDYLSVESVQKQF 658
RESULT 7
KAPC DROME STANDARD; PRT; 352 AA.
AC P12370; Q9VLY99;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE CAMP-dependent protein kinase catalytic subunit (EC 2.7.1.37) (PKA C).
GN PKA-C1 OR CDKA OR DCO OR CG4379.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88115281; PubMed=2828348;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-pfankoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Buser D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Foster J.C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko F., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nuskern D.J., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- ENZYME REGULATION: Activated by CAMP.
CC -!- SUBUNIT: Composed of two regulatory chains and two catalytic
CC chains.
CC -!- TISSUE SPECIFICITY: More abundant in adult head than adult body.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CAMP
CC subfamily.
CC
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CC -----
CC EMBL; M18655; AAA28412.1; --
CC EMBL; X16969; CAA34840.1; --
CC EMBL; AE003625; AAF52797.1; --
DR DR
DR SEQUENCE FROM N.A.
RX MEDLINE=88115281; PubMed=2828348;
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DR PIR; C31751; C31751.  
DR HSP; P05132; IATP.  
DR FlyBase; FBgn0000273; Pka-C1.  
DR GO; GO:0005886; C:plasma membrane; IDA.  
DR GO; GO:0007448; P:anterior/posterior pattern formation, imagi. . .; IMP.  
DR GO; GO:0015933; P:CAMP-mediated signaling; NAS.  
DR GO; GO:0007456; P:eye morphogenesis (sensu Drosophila); NAS.  
DR GO; GO:0007292; P:female gamete generation; IMP.  
DR GO; GO:0007611; P:learning and/or memory; NAS.  
DR GO; GO:0007480; P:leg morphogenesis (sensu Holometabola); NAS.  
DR GO; GO:0045475; P:locomotor rhythm; NAS.  
DR GO; GO:0008355; P:olfactory learning; NAS.  
DR GO; GO:0007314; P:occyte anterior/posterior axis determination; IMP.  
DR GO; GO:0008103; P:occyte microtubule cytoskeleton polarization; IMP.  
DR GO; GO:0008359; P:regulation of bicoid mRNA localization; IMP.  
DR GO; GO:0007317; P:regulation of pole plasm oskar mRNA localiz. . .; IMP.  
DR GO; GO:0045473; P:response to ethanol (sensu Insecta); NAS.  
DR GO; GO:0007622; P:rhythmic behavior; IMP.  
DR GO; GO:0007476; P:wing morphogenesis; IMP.  
DR InterPro; IPR000961; Pkinase C.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00869; pkinase; 1.  
DR Pfam; PF00433; pkinase C; 1.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TKG; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
DR TRANSFERASE; Serine/threonine-protein kinase; ATP-binding; CAMP;  
KIN Phosphorylation; Myristate; Lipoprotein.  
FE INIT MET 0 0 BY SIMILARITY  
FE LIPID 1 1 N-myristoyl glycine (By similarity).  
FE DOMAIN 45 299 PROTEIN KINASE.  
FE NP\_BIND 51 59 ATP (BY SIMILARITY).  
FE BINDING 74 74 ATP (BY SIMILARITY).  
FE ACT\_SITE 168 168 BY SIMILARITY.  
FE SEQUENCE 352 AA; 40707 MW; 88E42BCFA95E9640 CRC64;  
Very Match 24.2%; Score 521.5; DB 1; Length 352;  
Local Similarity 34.7%; Pred. No. 4.7e-28;  
Matches 111; Conservative 73; Mismatches 117; Indels 19; Gaps 6;  
21 DFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKCKVERNEVENFVKELQIMQGLEH 80  
43 DDFERIKITGSGFGRVMIVQHKPTKDYKAMKILDKQKVKLQKVQVHTLNKRILQIQF 102  
81 PELVNLWYGFQDEEDMFVMDLLGLGDLRYHLQONVHFKEETVKLFICBLVMDLYLQNG 140  
103 PELVSLRYHFHFKNSNLVWLVYVPGGEMFSLRKVKGRFSEPHSRFYAAQIVLAFAYLHYL 162  
141 RIHRDMKPDNILLDEGHVHTIDFNIAWLPRETOITWAGTKPYNAPEMSSRKAGY 200  
163 DLTYRDLKPENLILDSQGLVKVTDGFAKRVKGR--WTLCGTPPEYLAPEILSK---GY 217  
201 SFADVMSLGVATYELLGRGRPHIRSSSTSSKSEIVHTEITV---VTYPSAMSQEMVSLI 257  
218 NKAVDWWALGVLYEMAAAGYPPFF-----ADQFIQIYKIVSGKRVKRFPSFGSDKDLL 271  
258 KLLLENPPQRFSQL-----SDVQNFYFMDINWDVAFQKRLIPGFIPN-KGRNLCDPTFE 312  
272 RNLQVLDLTRYKNGAKAGVNDIKNQKFASTWDIAIPQKKIEAPFIPCRCKGPGDTNFD 331  
313 LEEMILESPLHKKKRLAK 332  
332 YEEALRISSTEKCAFEAE 351

RESULT 8

SKL1\_SCHPO STANDARD; PRT; 696 AA.  
AC P50530; Q9UTF3;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Serine/threonine-protein kinase sck1 (EC 2.7.1.37).  
GN SCK1 OR SPAC1B9.02C.  
OS Schizosaccharomyces pombe (Fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
OX NCBI\_TaxID=4896;  
[1]  
SEQUENCE FROM N.A.  
RX MEDLINE=96120227; PubMed=7498728;  
RA Jin M., Fujita M., Culley B., Apolinario E., Yamamoto M.,  
RA Maundrell K., Hoffman C.;  
RT "sck1, a high copy number suppressor of defects in the CAMP-dependent  
protein kinase pathway in fission yeast, encodes a protein homologous  
to the Saccharomyces cerevisiae SCH9 kinase.";  
RL Genetics 140:457-467(1995).  
[2]  
SEQUENCE FROM N.A.  
RN STRAIN=972;  
RC MEDLINE=21848401; PubMed=11859360;  
RX Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
RA Sgouros J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,  
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,  
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,  
RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,  
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,  
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,  
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,  
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Foraburg S.L.,  
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;  
RL "The genome sequence of Schizosaccharomyces pombe.";  
Nature 415:871-880(2002).  
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CAMP  
subfamily.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; D38108; BAA07286.1; -;  
DR EMBL; AL109951; CAB53053.1; -;  
DR PIR; S55694; S55694.  
DR HSP; P05132; IATP.  
DR GeneDB Spombe; SPAC1B9.02c; -;  
DR InterPro; IPR000008; C2.  
DR InterPro; IPR008973; C2\_CaLB.  
DR InterPro; IPR000961; Pkinase C.  
DR InterPro; IPR000719; Prot\_kinase.

DR InterPro; IPR008271; Ser thr\_pkin AS.  
 DR InterPro; IPR002290; Ser thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00168; C2; 1.  
 DR Pfam; PF00069; pkinase; 1.  
 DR Pfam; PF00433; pkinase C; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00239; C2; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00220; S\_TK; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 DR PROSITE; PS00109; PROTEIN KINASE ST; 1.  
 DR TRANSFERASE; Serine/threonine-protein kinase; ATP-binding; CAMP.  
 DR DOMAIN 302 563 PROTEIN KINASE.  
 DR NP\_BIND 308 316 ATP (BY SIMILARITY).  
 DR BINDING 331 331 ATP (BY SIMILARITY).  
 DR ACT\_SITE 428 428 BY SIMILARITY.  
 DR CONFLICT 199 199 A -> R (IN REF. 1).  
 DR SEQUENCE 696 AA; 78594 MW; A7B05F5BE4D42AF7 CRC64;  
 Query Match 24.2%; Score 519.5; DB 1; Length 696;  
 Best Local Similarity 37.2%; Pred. No. 1.4e-27;  
 Matches 112; Conservative 63; Mismatches 111; Indels 15; Gaps 7;  
 11 VEDENEDVNF--DFEILRAIGKSGFGKIVQKNDTKQMYAMKYNKQKVERNEVRNV 68  
 288 IYEHIEHVRGPEFTALRLIGKTFQGVLYVRNDINRIYAMKISKILVRKEVTH 347  
 69 FKEIQMGL---BHPFLVNLWYFQDEEMFMVVDLLGLDRLYHLQONVHKEETVKL 125  
 348 LGERNILVRLSDSPFTVGLKFSQFASDLYLTDMYSGGELFWHLQHEGRPFPEQRAKF 407  
 126 FICELVWALDYLNQRIHDMKPDNILLDEGHVHITDENIA-AMLPRETIITMAGTK 184  
 408 YIAELVLALEHLKHDIIYRLKPEINILLDADGHALCDLGLSKANLSANATTFPGTT 467  
 185 PYMAPEFSSKSGAGYSPAVDWSLGVTVAYELLGRRPYHIRSTSSKEIVHTFETTVT 244  
 468 EYLAEVLELDEK--GYTKQVDFNSLGVLFEMCCGWSFPY---APDVQMYRNIAFGKVR 522  
 245 YP-SAWSQMYSLKLEPNPQDFQSLSQSD---VONFPYVNDINWDVAFKRLIPGIP 300  
 523 FPKGLVLSSEGRSVRGLNRPNRLGAVDATTTELKEHPFFADINWDLSSKKVQPPFKP 582  
 301 N 301  
 583 N 583

RT "Cloning of a human insulin-stimulated protein kinase (ISPK-1) gene  
 RT and analysis of coding regions and mRNA levels of the ISPK-1 and the  
 RT protein phosphatase-1 genes in muscle from NIDDM patients.";   
 RL Diabetes 44:90-97 (1995).  
 RN [2]  
 RP SEQUENCE OF 2-582 FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=94189676; PubMed=8141249;  
 RA Moller D.E.; Xia C.-H.; Tang W.; Zhu A.X.; Jakubowski M.;  
 RT "Human risk isoforms: cloning and characterization of tissue-specific  
 RT expression.";  
 RL Am. J. Physiol. 266:C351-C359 (1994).  
 RN [3]  
 RP VARIANTS CLS VAL-75 AND ALA-227.  
 RX MEDLINE=97113410; PubMed=8955270;  
 RA Trivier E.; de Cesare D.; Jacquot S.; Pannetier S.; Zackai E.;  
 RT Young I.; Mandel J.-L.; Sassone-Corsi P.; Hanauer A.;  
 RT "Mutations in the kinase Rsk-2 associated with Coffin-Lowry  
 RT syndrome.";  
 RL Nature 384:567-570 (1996).  
 RN [4]  
 RP VARIANTS CLS PHE-82; GLN-127; TYR-154; VAL-225 AND ASP-431, AND  
 RP VARIANT SER-38.  
 RX MEDLINE=99057500; PubMed=9837815;  
 RA Jacquot S.; Merienne K.; de Cesare D.; Pannetier S.; Mandel J.-L.;  
 RA Sassone-Corsi P.; Hanauer A.;  
 RT "Mutation analysis of the RSK2 gene in Coffin-Lowry patients:  
 RT extensive allelic heterogeneity and a high rate of De novo  
 RT mutations.";  
 RL Am. J. Hum. Genet. 63:1631-1640 (1998).  
 RN [5]  
 RP VARIANTS CLS TRP-114 AND GLN-729.  
 RX MEDLINE=99191975; PubMed=10094187;  
 RA Abidi F.; Jacquot S.; Lassiter C.; Trivier E.; Hanauer A.;  
 RA Schwartz C.E.;  
 RT "Novel mutations in Rsk-2, the gene for Coffin-Lowry syndrome (CLS).";  
 RL Eur. J. Hum. Genet. 7:20-26 (1999).  
 CC -1- FUNCTION: Phosphorylates a wide range of substrates including  
 CC ribosomal protein S6. Implicated in the activation of the mitogen-  
 CC activated kinase cascade.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -1- TISSUE SPECIFICITY: Expressed in many tissues, highest levels in  
 CC skeletal muscle.  
 CC -1- DISEASE: Defects in RPS6KA3 are the cause of Coffin-Lowry syndrome  
 CC (CLS) [MIM:303600], an X-linked dominant disorder characterized by  
 CC severe mental retardation with facial and digital dysmorphisms,  
 CC and progressive skeletal deformations.  
 CC -1- SIMILARITY: Belongs to the Ser/thr family of protein kinases. S6  
 CC kinase subfamily.  
 CC  
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 CC  
 CC EMBL; U08316; AAA81952.1; -;  
 DR EMBL; L07599; AAC82495.1; -;  
 DR PIR; I38556; I38556.  
 DR HSP; O63450; 1A06.  
 DR Genew; HGNC:10432; RPS6KA3.  
 DR MIM; 300075; -;  
 DR MIM; 303600; -;  
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; TAS.  
 DR GO; GO:0007417; P:central nervous system development; TAS.  
 DR GO; GO:0007165; P:skeletal development; TAS.  
 DR GO; GO:0001501; P:skeletal development; TAS.  
 DR InterPro; IPR000961; Pkinase\_C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.



DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00069; pkinase; 2.  
DR PRINTS: PF00433; pkinase; C; 1.  
DR ProDom: PD000001; Prot\_kinase; 2.  
DR SMART: SM00133; S\_TK\_X; 1.  
DR SMART: SM00220; S\_TKG; 2.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 2.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 2.  
DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 2.  
DR TransFam: Serine/threonine-protein kinase; ATP-binding;  
KW Repeat; Multigene family; Disease mutation; Polymorphism.  
FT DOMAIN 68 327  
FT NP\_BIND 74 82  
FT BINDING 100 100  
FT ACT\_SITE 193 193  
FT NP\_BIND 428 436  
FT BINDING 451 451  
FT ACT\_SITE 539 539  
FT VARIANT 38 38  
FT VARIANT 75 75  
FT VARIANT 82 82  
FT VARIANT 114 114  
FT VARIANT 127 127  
FT VARIANT 154 154  
FT VARIANT 225 225  
FT VARIANT 227 227  
FT VARIANT 431 431  
FT VARIANT 729 729  
FT CONFLICT 424 424  
FT CONFLICT 480 480  
FT CONFLICT 494 494  
FT SEQUENCE 740 AA; 83736 MW; 486AE8357CEAB6C8 CRC64;  
Query Match 23.9%; Score 514.5; DB 1; Length 740;  
Best Local Similarity 35.8%; Pred. No. 3.3e-27;  
Matches 112; Conservative 65; Mismatches 117; Indels 19; Gaps 7;  
QY 11 VFDENEDVDFHFEILRAIGKSGFGKVCIVQK---NDTKQWYAMKYNKQKCVNERVNRN 67  
DB 56 VKEGHEKADPSQFELLKVLGGSGFGKVFVKYKISGSDARQLYAMKVLKATLKVRDRVRT 115  
QY 68 VFRELQIMQGLEHFFLVNLWYSQDEEDNFWVDLLGLGDLRLHQLQNVHFKEETVKLFI 127  
DB 116 KM-ERDILVEVNHPPFIVKLHVAFQTEGKLYLLDFLRGGDLFRLSKVMFTBEDVKFYL 174  
QY 128 CELVMALDYLVQNRIRHDMKPNILLDEGHVHITDFNIA-AMLPRETQITTMAGTKPY 186  
DB 175 AELALALDLHLSGLIYRDLKPNILLDEGHGKLTDFGLSKESIDHEKAYFCGTVVEY 234  
QY 187 MAPEMFSRRKAGYSFPAVDNWSLGVATYELLRRGRPYHRSSTSSSSKEIVHTFTTVVTP 246  
DB 235 MAPEVNRR---GHQSQADWWSFGLVFMELTGLTFP---QGDKRKETMTMILKAKLGMP 288  
QY 247 SANSQEMVSLIKLLEPNPQRFQSQ-----LSDVQNFYMDNDINWDAVQKRLPGFTPNK 302  
DB 289 QFLSPEAQSLRLMLFKRNPNKLGAGPDGVBEIKRHGFFSTIDWNKLYRREIHPPFPKAT 348  
QY 303 GR----LNCDDTF 311  
DB 349 GRPDTYTFDFPEF 361

RESULT 10  
K6A3 MOUSE  
ID K6A3 MOUSE STANDARD; PRT; 740 AA.  
AC P18654; Q03140; Q8K3J8;  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Ribosomal protein S6 kinase alpha 3 (EC 2.7.1.37) (S6K-alpha 3) (90  
DE kDa ribosomal protein S6 kinase 3) (p90-RSK 3) (Ribosomal S6 kinase 2)  
DE (RSK-2) (pp90RSK2) (MAP kinase-activated protein kinase 1b)  
DE (MAPKAPK1B).  
GN RPS6KA3 OR RSK2 OR RPS6KA-RS1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP PubMed=12016217;  
RX Chrestensen C.A., Sturgill T.W.;  
RT "Characterization of the p90 ribosomal S6 kinase 2 carboxyl-terminal  
RT domain as a protein kinase.";  
RL J. Biol. Chem. 277:27733-27741 (2002).  
RN [2]  
RN SEQUENCE OF 108-740 FROM N.A.  
RP MEDLINE=89384612; PubMed=2779569;  
RX Alcorn D.A., Crews C.M., Sweet L.J., Bankston L., Jones S.W.,  
RA Erikson R.L.;  
RT "Sequence and expression of chicken and mouse rsk: homologs of  
RT Xenopus laevis ribosomal S6 kinase.";  
RL Mol. Cell. Biol. 9:3850-3859 (1989).  
CC -!- FUNCTION: Serine/threonine kinase that may play a role in  
CC mediating the growth-factor and stress induced activation of the  
CC transcription factor CREB (By similarity).  
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -!- COFACTOR: Magnesium (By similarity).  
CC -!- ENZYME REGULATION: Activated by multiple phosphorylations on  
CC threonine and serine residues (By similarity).  
CC -!- SUBUNIT: Forms a complex with either ERK1 or ERK2 in quiescent  
CC cells. Transiently dissociates following mitogenic stimulation (By  
CC similarity).  
CC -!- TISSUE SPECIFICITY: Intestine, thymus, lung, heart and brain.  
CC -!- PTM: Autophosphorylated on Ser-386, as part of the activation  
CC process (By similarity).  
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. S6  
CC kinase subfamily.  
CC  
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CC  
CC EMBL; AY083469; AAM00022.1; --  
DR PIR; C32571; C32571.  
DR PIR; S30504; S30504.  
DR HSP; C63450; 1A06.  
DR MGD; MGI:104557; Rps6ka3.  
DR GO; GO:0004674; P; protein serine/threonine kinase activity; IDA.  
DR InterPro; IPR000961; Pkinase.C.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; pkinase; 2.  
DR Pfam; PF00433; pkinase; C; 1.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD000001; Prot\_kinase; 2.  
DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TKG; 2.



SEQUENCE FROM N.A.  
STRAIN=JR26-19D; PubMed=8442384;  
MEDLINE=93182331; PubMed=8442384;  
de Blasi F., Carra E., de Vendittis E., Masturzo P., Burderi E.,  
Lambrioudaki I., Mirisola M.G., Seidita G., Fasano O.;  
"The SCH9 protein kinase mRNA contains a long 5' leader with a small  
open reading frame.";  
Yeast 9:21-32(1993).  
[3]

SEQUENCE FROM N.A.  
STRAIN=G288c / AB972;  
MEDLINE=94378003; PubMed=8091229;  
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,  
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,  
Kucaba T., Hillier L.W., Jlier M., Johnston L., Langston Y.,  
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,  
Nhan M., Rifkin L., Riles L., St Peter H., Trevasakis E., Vaughan K.,  
Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,  
Vaundt M.;  
"Complete nucleotide sequence of Saccharomyces cerevisiae chromosome  
VIII.";  
Science 265:2077-2082(1994).

-I- FUNCTION: Protein kinase that is part of growth control pathway  
which is at least partially redundant with the cAMP pathway.  
-I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
-I- ENZYME REGULATION: Activated by cAMP.  
-I- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. cAMP  
subfamily.  
-I- SIMILARITY: Contains 1 C2 domain.

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EMBL; X12560; CAA31073.1; --  
EMBL; X57629; CAA40853.1; ALT\_INIT.  
EMBL; U00029; AAB69735.1; --  
PIR; S48986; S48986.  
HSSP; P05132; IFMO.  
GermOnline; I39523; --  
SGD; S0001248; SCH9.  
GO; GC:0004674; F:protein serine/threonine kinase activity; IGI.  
GO; GC:0007574; P:cell aging (sensu Saccharomyces); IMP.  
GO; GC:0006468; P:protein amino acid phosphorylation; IGI.  
GO; GC:0008361; P:regulation of cell size; IDA.  
InterPro; IPR000008; C2.  
InterPro; IPR008973; C2\_CaLB.  
InterPro; IPR000961; Pkinase\_C.  
InterPro; IPR000719; Prot\_kinase.  
InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
InterPro; IPR002290; Ser\_thr\_pkinase.  
Pfam; PF00168; C2; 1.  
Pfam; PF00069; Pkinase; 1.  
Pfam; PF00433; pkinase\_C; 1.  
ProDom; PD000001; Prot\_kinase; 1.  
SMART; SM00239; C2; 1.  
SMART; SM00133; S\_TK\_X; 1.  
SMART; SM00220; S\_TKG; 1.  
PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
PROSITE; PS00109; PROTEIN\_KINASE\_ST; 1.  
PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
PROSITE; PS00044; C2\_DOMAIN\_2; FALSE\_NEG.  
Transfaser; Serine/threonine-protein kinase; ATP-binding; cAMP.  
FT DOMAIN 226 266 ASN-RICH.  
FT DOMAIN 319 360 C2 DOMAIN.  
FT DOMAIN 411 670 PROTEIN KINASE.  
FT NP BIND 417 425 ATP (BY SIMILARITY).  
FT BINDING 440 440 ATP (BY SIMILARITY).  
FT ACT SITE 537 537 BY SIMILARITY.

-|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
-|- SUBUNIT: Composed of two regulatory chains and two catalytic chains.

-|- ALTERNATIVE PRODUCTS:  
Event=Alternative splicing; Named isoforms=l3;  
Comment=Experimental confirmation may be lacking for some isoforms;

Name=e;  
IsoId=P21137-1; Sequence=Displayed;  
Name=a; Synonyms=Major;  
IsoId=P21137-2; Sequence=VSP\_004751, VSP\_004758;  
Name=b; Synonyms=Minor;  
IsoId=P21137-3; Sequence=VSP\_004751;  
Name=c;  
IsoId=P21137-4; Sequence=VSP\_004756, VSP\_004757;  
Name=d;  
IsoId=P21137-5; Sequence=VSP\_004750;  
Name=f;  
IsoId=P21137-6; Sequence=VSP\_004752, VSP\_004758;  
Name=g;  
IsoId=P21137-7; Sequence=VSP\_004754, VSP\_004758;  
Name=h;  
IsoId=P21137-8; Sequence=VSP\_004753, VSP\_004758;  
Name=i;  
IsoId=P21137-9; Sequence=VSP\_004754;  
Name=j;  
IsoId=P21137-10; Sequence=VSP\_004753;  
Name=k;  
IsoId=P21137-11; Sequence=VSP\_004755;  
Name=l;  
IsoId=P21137-12; Sequence=VSP\_004758;  
Name=m;  
IsoId=P21137-13; Sequence=VSP\_004750, VSP\_004758;

-|- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CAMP subfamily.

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EMBL; M37119; AAAS1610.1; -.  
EMBL; M37114; AAAS1610.1; JOINED.  
EMBL; M37115; AAAS1610.1; JOINED.  
EMBL; M37116; AAAS1610.1; JOINED.  
EMBL; M37117; AAAS1610.1; JOINED.  
EMBL; M37118; AAAS1610.1; JOINED.  
EMBL; Z32096; CAD45613.1; -.  
EMBL; Z32096; CAD45614.1; -.  
EMBL; Z32096; CAD45615.1; -.  
EMBL; Z32096; CAD45616.1; -.  
EMBL; Z31511; CAD45616.1; JOINED.  
EMBL; Z32096; CAD45617.1; -.  
EMBL; Z31511; CAD45617.1; JOINED.  
EMBL; Z32096; CAD45618.1; -.  
EMBL; Z31511; CAD45618.1; JOINED.  
EMBL; Z32096; CAD45619.1; -.  
EMBL; Z31511; CAD45619.1; JOINED.  
EMBL; Z32096; CAD45620.1; -.  
EMBL; Z31511; CAD45620.1; JOINED.  
EMBL; Z32096; CAD45621.1; -.  
EMBL; Z31511; CAD45621.1; JOINED.  
EMBL; Z32096; CAD45622.1; -.  
EMBL; Z31511; CAD45622.1; JOINED.  
EMBL; Z32096; CAD45623.1; -.  
EMBL; Z31511; CAD45623.1; JOINED.  
EMBL; Z32096; CAB05034.1; -.  
EMBL; Z31511; CAB05034.1; JOINED.  
EMBL; Z32096; CAB05035.1; -.  
EMBL; Z31511; CAB05035.1; JOINED.

[illegible]

DB	445	AELLCALDSLHLVDIYRDLPENILLDYQGHIALCDFGLCKLNKMDKTDFTOCTPEY	508
QY	187	MAPEMFSRKGAGYFAVDWWSLGVAYELLGRPHYIRS-STSSKEIVHTFETVTVY	245
DB	509	LAPBIL---LQGYTKTVDWTLGLLYEMMTGLPPYDENVPVVMYKILQ-----QPLLF	561
QY	246	PSAWSQEMVSLKKLEPNPDRF--SLSVDQVFPYMNNDINWDAVFKRLIPGPIPNKG	303
DB	562	PDGFDPAKOLLIGLLSRDPSRRLGVTGTDIRNHPFFKDISW---KLLKLGYP---	614
QY	304	RINCPTPELEBEEMILESPLHKKKKLAKKMKDCDSSQTCLLQEHLD-SVQKEF	359
DB	615	-----PYKPIVKSEIDTANFQDEFTK-EKPIDSVVDEYLSASIQOKF	655
RESULT 14			
KAPA CRIGR STANDARD; PRT; 350 AA.			
ID	KAPA CRIGR	STANDARD; PRT; 350 AA.	
AC	P25321;		
DT	01-MAY-1992 (Rel. 22, Created)		
DT	01-MAY-1992 (Rel. 22, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	CAMP-dependent protein kinase, alpha-catalytic subunit (EC 2.7.1.37)		
DE	(PKA C-alpha).		
GN	PRKACA.		
OS	Cricetulus griseus (Chinese hamster).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;		
OC	Cricetulus.		
OX	NCBI_TaxID=10029;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE=91244783; PubMed=1645343;		
RA	Howard P., Day K.H., Kim K.E., Richardson J., Thomas J., Abraham I.,		
RA	Fleischmann R.D., Gottesman M.M., Maurer R.A.;		
RT	"Decreased catalytic subunit mRNA levels and altered catalytic		
RT	subunit mRNA structure in a CAMP-resistant Chinese hamster ovary cell		
RT	line.";		
RL	J. Biol. Chem. 266:10189-10195 (1991).		
CC	-!- FUNCTION: Phosphorylates a large number of substrates in the		
CC	cytoplasm and the nucleus.		
CC	-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.		
CC	-!- ENZYME REGULATION: Activated by CAMP.		
CC	-!- SUBUNIT: A number of inactive tetrameric holoenzymes are produced		
CC	by the combination of homo- or heterodimers of the different		
CC	regulatory subunits associated with two catalytic subunits. CAMP		
CC	causes the dissociation of the inactive holoenzyme into a dimer of		
CC	regulatory subunits bound to four CAMP and two free monomeric		
CC	catalytic subunits.		
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic (inactive holoenzyme and		
CC	monomeric catalytic subunit). Translocates into the nucleus		
CC	(monomeric catalytic subunit) (By similarity).		
CC	-!- TISSUE SPECIFICITY: Ubiquitously expressed in mammalian tissues.		
CC	-!- PTM: Asn-2 is partially deaminated to Asp-2 giving rise to 2		
CC	major isoelectric variants, called CB and CA respectively (By		
CC	similarity).		
CC	-!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.		
CC	CAMP subfamily.		
-----			
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or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
-----			
DB	EMBL; M63311; AAA37010.1; -		
DR	HSP; B40384; OHYCA.		
DR	HSP; P05132; ICTP.		
DR	InterPro; IPR000961; Pkinase C.		
DR	InterPro; IPR000719; Prot kinase.		
DR	InterPro; IPR006271; Ser_thr_pkin_AS.		

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10 Search completed: May 26, 2004, 20:18:50  
Job time : 19 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: May 26, 2004, 20:15:43 ; Search time 20 Seconds  
(without alignments)  
1957.498 Million cell updates/sec

Title: US-10-620-845-9  
Perfect score: 2151  
Sequence: 1 MGATSKRPVFDENEDVNF.....VTNGQMDTGLSETFQTSKVS 407

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Sequenced: 283366 seqs, 96191526 residues  
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_78.\*  
1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Rank	Score	Match	Length	DB	ID	Description
1	852.5	39.6	379	2	T23688	hypothetical prote
2	546	25.4	479	2	A38578	protein kinase 2 (
3	537.5	25.0	648	1	J01150	protein kinase (EC
4	534	24.8	480	2	S56639	ribosomal protein
5	529.5	24.6	465	2	S68462	protein kinase ATP
6	526	24.5	680	2	S37955	protein kinase YPK
7	521.5	24.2	353	2	C31751	protein kinase (EC
8	521	24.2	471	2	S68463	protein kinase ATP
9	519.5	24.2	696	2	S55694	protein kinase (EC
10	519.5	24.2	785	2	T20232	hypothetical prote
11	518	24.1	352	2	S19027	protein kinase A (
12	517	24.0	359	2	T21211	hypothetical prote
13	514.5	23.9	740	2	I38556	ribosomal protein
14	514.5	23.9	823	2	S48986	probable protein k
15	514	23.9	375	2	T21212	hypothetical prote
16	514	23.9	677	2	J00178	protein kinase YKR
17	513.5	23.9	351	1	OKHYCA	protein kinase (EC
18	513.5	23.9	733	2	A57459	ribosomal protein
19	512.5	23.8	360	1	OKHUCG	protein kinase (EC
20	510	23.7	359	1	OKKWC1	protein kinase (EC
21	509.5	23.7	351	1	OKHU2C	protein kinase (EC
22	509.5	23.7	351	1	OKRT2C	protein kinase (EC
23	508.5	23.6	587	2	A53758	protein kinase C (
24	508.5	23.6	586	2	A49509	protein kinase C (
25	507.5	23.6	351	1	OKBO2C	protein kinase (EC
26	507.5	23.6	752	1	A32571	ribosomal protein
27	507	23.6	351	1	OKRT5C	protein kinase (EC
28	507	23.6	351	1	OKMSCB	protein kinase (EC
29	507	23.6	351	1	OKHYCB	protein kinase (EC

RESULT 1  
T23688  
hypothetical protein M03C11.1 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 31-Jan-2000  
C;Accession: T23688  
R;McMurray, A.  
submitted to the EMBL Data Library, April 1995  
A;Reference number: Z19783  
A;Accession: T23688  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-379 <WIL>  
A;Cross-references: EMBL:Z49128; PIDN:CRA89953.1; GSPDB:GN00021; CESP:M03C11.1  
A;Experimental source: clone M03C11  
C;Genetics:  
A;Gene: CESP:M03C11.1  
A;Map position: 3  
A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3  
C;Superfamily: kinase-related transforming protein; protein kinase homology

ALIGNMENTS

Query Match	39.6%; Score 852.5; DB 2; Length 379;
Best Local Similarity	44.4%; Pred. No. 8.1e-32;
Matches	159; Conservative 70; Mismatches 116; Indels 13; Gaps 4;
Qy	22 HFEITLRAIGKSGKVCIVOKNDTKKYYAMKYNKQKVERNEVNFVKELQIMQGLEHP 81
Db	27 HFSVIRSIGRGAFGKVCIVQERTKTKYFALKYMKNRCEIKGVAANVIRELTLLSKMSHP 86
Qy	82 FLVNLWYSFQDEEDMFVMDLLGLGDLRYHLQNVHFKEETVKLFCILVMALDYLNQR 141
Db	87 FIVNLWTFQDGYMYMVSLLGLGDLRYHLQNVHFKEETVKLFCILVMALDYLNQR 146
Qy	142 IIRDMKPDNILLDEHGHVHTFNIAAMLPRETQITTMAGTKPYMAPEMFSS--RKAG 199
Db	147 IVHRDIKPNILLDEHGHVHTFNIAAMLPRETQITTMAGTKPYMAPEMFSS--RKAG 206
Qy	200 YSEAVDMSLGVYAYELLGRPPYHRSSTSSKEIVHTFTVTVTVPYSAQSQEVLK 259
Db	207 YDSKVDVWALGVCFYEMLRGKTPFESSRTPKEAYVAFRESSIPYFAHPTDDIQINS 266
Qy	260 LLEPNPQRFSQLSDVQNFPMNDINMDAVFQKRLIPGFIPNKGRLNCDPTFELEEMILE 319
Db	267 MLKFDKRLVGLAIAKKHSYTERIDFKSVFEKPSVPFIPCKEGLNCDPMYLEERILV 326
Qy	320 SKPLHKKKKLAKKEDMKRCDSSQTCCLQEHLDVQKEFIIFNREKVNKRDENKRNQ 377
Db	327 STPIH--RRRTNHNSSGRSSSEPPQNAALVE---VSKAFIDFSRHNV-----KIEPN 373

RESULT 2  
A38578

protein kinase 2 (EC 2.7.1.1) - slime mold (Dictyostelium discoideum)  
 C:Species: Dictyostelium discoideum  
 C:Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 24-Sep-1999  
 C:Accession: A38578  
 R:Haribabu, B.; Dotti, R.P.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 11115-11119, 1991  
 A:Title: Identification of a protein kinase multigene family of Dictyostelium discoideum  
 A:Reference number: A38578; MUID:91142122; PMID:1996312  
 A:Accession: A38578  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-479 <HAR>  
 A:Cross-references: GB:M59744; NID:g167717; PIDN:AAA33186.1; PID:g167718  
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog  
 C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonine  
 F:451-407/Domain: protein kinase homology <KIN>  
 F:439-167/Region: protein kinase ATP-binding motif

Query Match 25.4%; Score 546; DB 2; Length 479;  
 Best Local Similarity 36.5%; Pred. No. 5.2e-18;  
 Matches 118; Conservative 66; Mismatches 123; Indels 16; Gaps 6;

11 VPEN EDVNFDPHEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKVERNEVRNV 69  
 140 IFKKNQSAKDDFELLNVIGKSGFKVMQVKKGDKIPAMKVLKDAIARQVNHK 199  
 70 KELQIMQGLEHPLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHKEETVKLFCE 129  
 200 SEKITLQCTSHPPFVNLHYAFQKDLVLDLVFNGGELFFHLKRGREFEPNRYIAE 259  
 130 LVNMDLYLQNRILHDMKPDNILLDEHGHVHTDFNIAAMLPRETOITTMAGTKPYMAP 189  
 260 IVGALDHLHKQDIVYRDLKPEILLDSSEGHICITDFGLSKKIETTDGTFTFCGTPEYLAP 319  
 190 EMPSSRKAGYSFADVWNSLGVYAYELLRRGRPPYHRSSTSSKEIVHTFTTIVTTPSAW 249  
 320 EVLN--GHGHCADVWNSLGLTLLYEMLTGLPPYSQVNTMYQKILNGLSKIPTV--I 373  
 250 SQEMVSLKLLKLEPNPDQRFSQL--SDVQNFPMNDINWDVAFQKRLIPGFIP---NKG 303  
 374 SPEAKSLLEGILLTREVDRKLTGKGGEVKQHPKFNIDWEKLRKEVEVHFKVKSQGTD 433  
 304 RLNCDDPTFELE--EMILESKEPL 323  
 434 ISQIDPVFTQERPMDLSVETSA 456

RESULT 3  
 350  
 protein kinase (EC 2.7.1.37) CAMP-dependent, catalytic chain - slime mold (Dictyostelium  
 C:Species: Dictyostelium discoideum  
 C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 24-Apr-1998  
 C:Accession: JQ1150  
 R:Buergi, E.; Anjard, C.; Scholder, J.C.; Raymond, C.D.  
 Gene 102, 57-65, 1991  
 A:Title: Isolation of two genes encoding putative protein kinases regulated during Dicty  
 A:Reference number: JQ1150; MUID:91323730; PMID:1864510  
 A:Accession: JQ1150  
 A:Molecule type: DNA  
 A:Residues: 1-648 <BUE>  
 A:Cross-references: GB:M38703  
 C:Genetics:  
 A:Gene: PK2  
 A:Introns: 578/3  
 C:Complex: heterodimer with regulatory chain; active catalytic chain is released when ca  
 C:Function:  
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
 A:Note: important for cell type differentiation and fruiting body morphogenesis  
 C:Superfamily: Dictyostelium CAMP-dependent protein kinase catalytic chain; protein kina  
 C:Keywords: ATP; magnesium; phosphoprotein; phosphotransferase; serine/threonine-specifi  
 F:126-223/Region: glutamine-rich  
 F:297-312/Region: glutamine-rich  
 F:334-590/Domain: protein kinase homology <KIN>

F:342-350/Region: protein kinase ATP-binding motif  
 F:365,384,459,461/Active site: Lys, Glu, Asp, Lys #status predicted  
 F:464,468/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 25.0%; Score 537.5; DB 1; Length 648;  
 Best Local Similarity 34.1%; Pred. No. 1.6e-17;  
 Matches 109; Conservative 74; Mismatches 120; Indels 17; Gaps 6;

9 PPVFEDENEDVNFDPHEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKVERNEVRNV 68  
 325 PPV--NARERLKEFKQIRVLGTGFGKYLQNTQKDGCCYAYKCLNKAYVVLQKQVEHL 381  
 69 FXELQIMQGLEHPLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHKEETVKLFIC 128  
 382 NSEKSLSSIIHPPFVNLVYQAFQDEKKLYLLPEYVAGGEVFTHLRKSMTFSNTAKFYAA 441  
 129 ELVMDLYLQNRILHDMKPDNILLDEHGHVHTDFNIAAMLPRETOITTMAGTKPYMA 188  
 442 EIVALEFLHKQIVYRDLKPEILLDSQGHKIDTDFGAKRV--EDRTFTLCGTPEYLA 499  
 189 PEMFSSRKAGYSFADVWNSLGVYAYELLRRGRPPYHRSSTSSKEIVHTFTTIVTTPSA 248  
 500 PEIIQSK---GHGKADVWNSLGLTLLYEMLTGLPPYSQVNTMYQKILNGLSKIPTV 553  
 249 WSOEMVSLKLLKLEPNPDQRFSQLS---DVQNFPMNDINWDVAFQKRLIPGFIPNKG 304  
 554 FQVDADKDLIKLLTADRTTRRLGALKDGLDVKNHRWFSINWERYLQRRDNGPFIKIQH 613  
 305 LNCDDPTFELE--EMILESKEP 322  
 614 QGDSSNFEMVDEEMVEEPP 633

RESULT 4  
 S56639  
 ribosomal protein S6 kinase homolog (clone AspK11) - oat  
 N:Alternate names: mitogen-activated protein kinase pp70 homolog  
 C:Species: Avena sativa (oat)  
 C:Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 24-Sep-1999  
 C:Accession: S56639  
 R:Huttly, A.K.; Phillips, A.L.  
 Plant Mol. Biol. 27, 1043-1052, 1995  
 A:Title: Gibberellin-regulated expression in oat aleurone cells of two kinases that show  
 A:Reference number: S56638; MUID:95284341; PMID:7766874  
 A:Accession: S56639  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-480 <HUT>  
 A:Cross-references: EMBL:X79992; NID:g871985; PIDN:CAA56313.1; PID:g871986  
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog  
 C:Keywords: ATP; phosphotransferase; protein kinase  
 F:149-407/Domain: protein kinase homology <KIN>  
 F:157-165/Region: protein kinase ATP-binding motif

Query Match 24.8%; Score 534; DB 2; Length 480;  
 Best Local Similarity 36.0%; Pred. No. 1.8e-17;  
 Matches 109; Conservative 61; Mismatches 123; Indels 10; Gaps 3;

14 ENEDVNFDPHEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKVERNEVRNVFKELQ 73  
 142 ENEAUGLDNFELVLUKVGQAGFGVYVRMKGTSEITAMKVRKDKILEKNHAYMYKAERD 201  
 74 IMQGLEHPLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHKEETVKLFICELVMA 133  
 202 ILTKVDHPFVQLRYSFQTKRYRLVLDLVFNGGELFFHLKRGREFEPNRYIAEIVSA 261  
 134 LDVQLQNRILHDMKPDNILLDEHGHVHTDFNIAAMLPRETOITTMAGTKPYMAEMFS 193  
 262 VAHLHANGIMHRLDKPENILLDARGHMLTDFGLAKEPFDENTRSNMGCGTVEYNAPEIV- 320  
 154 SRKAGYSFADVWNSLGVYAYELLRRGRPPYHRSSTSSKEIVHTFTTIVTTPSAEQEM 253  
 321 --QGRGDKAADWNSVGLLFFELMTGKPPFF---GGRDKIQKIIVREKMKLPSYLSSEV 375



R.Ramezani Rad, M.; Xu, G.; Kirchrath, L.; Fritz, C.; Keuchel, H.; Hollenberg, C.P.  
submitted to the Protein Sequence Database, March 1994  
A:Reference number: S37953  
A:Accession: S37955  
A:Molecule type: DNA  
A:Residues: 1-680 <RAM>  
A:Cross-references: EMBL:Z28126; NID:g486212; PIDN:CAA81967.1; PID:g486213; MIPS:YKL126W  
A:Experimental source: strain S288C  
R:Maaurer, R.A.  
DNA 7, 469-474, 1988  
A:A:Title: Isolation of a yeast protein kinase gene by screening with a mammalian protein  
A:Reference number: A31248; MUID:89090805; PMID:2850145  
A:Accession: A31248  
A:Molecule type: DNA  
A:Residues: 1-200, 'L', 202-552, 'I', 554-680 <MAU>  
A:Cross-references: EMBL:M21307; NID:g172180; PIDN:AAA34880.1; PID:g172181  
R:Chen, P.; Lee, K.S.; Levin, D.E.  
Mol. Gen. Genet. 236, 443-447, 1993  
A:Title: A pair of putative protein kinase genes (YPK1 and YPK2) is required for cell growth  
A:Reference number: S30903; MUID:93173125; PMID:8437590  
A:Accession: S30903  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-200, 'L', 202-226, 'T', 228-552, 'I', 554-680 <CHE>  
C:Genetics:  
A:Gene: SGD:YPK1  
A:Cross-references: SGD:S0001609; MIPS:YKL126W  
A:Map position: 11L  
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homologs  
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase  
F:345-602/Domain: protein kinase homology <KN>  
F:353-361/Region: protein kinase ATP-binding motif  
F:470/Active site: Asp #status predicted

Query Match	24.5%;	Score 526;	DB 2;	Length 680;
Best Local Similarity	32.6%;	Pred. No. 5.6e-17;		
Matches 1..7;	Conservative	77;	Mismatches 123;	Indels 42; Gaps 10;

QY	8	KPVFDENEVDNFDFEILRAIGKSGPKVILVQKNDTKMYAMKMKQCKVERNEVRN	67
Db	335	KP---SRNKPLSIDDFLLKVIKSGFGKVMQVRKKDTQKVYALKAIRKSYIVSKSEVTH	391
QY	68	VPKELQIQGLEHPEFLNLYWSFQDEEMFMVVDLLGGDLRYHLQONVHFKEETVKLFI	127
Db	392	TLAERTVLARVDCPFI VPLKFSQSPKLYFVLAFINGELFYHLQKEGRFDLSRAFYT	451
QY	128	CELVMAIDYLQNRIRHDKPDNILLDEHGHVHTIDFNIAAMLPRETOIT-TMAGTKPY	186
Db	452	AEILCALDNLHLKLDVVYEDLAKPENILDDYQGHIALCDFGLCKLNKDKDDTDTFCGTPEY	511
QY	187	MAPMFSRRKAGYSFAVDWNSLGVTAELLRCRRPYHRSSTSSKEIVHFTFTTV---V	243
Db	512	LAPEL---LGLGYTKAVDWTGLVLLYEMLTGLPPY-----DEDVPMYKKILQEP	562
QY	244	TPYSAWQEWVSLAKLLEPNPQDQ--FSQLSDVQNFYMYNDINMDAVFQRLIPGFI	301
Db	563	VFPDGFORDAKDLIGLRSRPTRLGNGADEIRNHPFSQLSWKRLMKGIYPYKPA	622
QY	302	KGRNLNCDPTFEELSEEMILESPLHKKKRIAKKEKMKRCKDSSQTCILQELH-DVQKEF	359
Db	623	VS---NSMDTSNDFDEFTREKI-----DS-----VVDEVLSSEVQKQF	658

RESULT 7  
C31751  
protein kinase (EC 2.7.1.37), cAMP-dependent, catalytic chain - fruit fly (Drosophila mel)  
C:Species: Drosophila melanogaster  
C:Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 18-Jun-1999  
C:Accession: C31751; A28269  
R:Kalderon, D.; Rubin, G.M.  
Genes Dev. 2, 1539-1556, 1988  
A:Title: Isolation and characterization of Drosophila cAMP-dependent protein kinase genes  
A:Reference number: A31751; MUID:89107990; PMID:3215511

[illegible]

288 IYEHIEHVRGPEFTALRLIGKGTQGVYLRKNDNTRIYAMKSKLIVRKKEVHT 347  
69 FKELOINMOGL---EHPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVHKEEIVKL 125  
348 LGERNILVRLSLDESPITGLKFSQFASDLYLLTDTMSGGLFWMHLOHGRPEQRAKF 407  
126 FICELVMDLYLQORIIRHMDKPNILLDEHGHVHTDANIA-AMPLPRETQITTMAGTK 184  
408 YIALVLALEHLHKKHDIYRDLKPEKILLDDGHALCDGFLSKANLSANATNTFCGTT 467  
185 PYMAPENFSSKAGYGFAPVDMWSLGVYATYELLGRPPYHRSSTSKKEIVHTPETTVT 244  
468 EYLAPEVLEDK---GYTKQVDFMSLGVLPFEMCCGWSPPY---APDVQOQYRNIAFGKVR 522  
245 YP-SAWSQEWVSLKLEPNPDORFQSLSP---VQNPFPYNDINMDAVFQKRLIPGIP 300  
523 FPKGLVSGSEGRFVRLNRPNRLGAVDTTELKHPFFADINWDLKSKVQPPFPK 582  
301 N 301  
583 N 583  
Query Match 24.2%; Score 519.5; DB 2; Length 785;  
Best Local Similarity 37.0%; Pred. No. 1.2e-16;  
Matches 111; Conservative 72; Mismatches 106; Indels 11; Gaps 8;  
14 ENEDVNFDFEITLRAIGKSGFGKVCIVQ---NDTKMYAMKYNKQKCVNERNE-VRNVF 69  
8 EGEKVMENFALLRVLGKAGYKGVFLVRKVGKDHNTIYAMKVLKTRVLTQKULEHTM 67  
70 KEOLOINMOGLE-HPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVHKEEIVKLFC 128  
68 AERQVLERLRGTFFLVNFYAFQDTKLHVMYVARGGELFTHLCRSGHFDLEAARFVIA 127  
129 ELVMDLYLQORIIRHMDKPNILLDEHGHVHTDANIA-AMPLPRETQITTMAGTKPY 186  
128 ELVVAIDSLHQRKVIYRDLKLENILLDEHGHVHTDANIA-AMPLPRETQITTMAGTKPY 187  
187 MAPENFSSKAGYGFAPVDMWSLGVYATYELLGRPPYHRSSTSKKEIVHTPETTVT 245  
188 MSPENVRNREG-GYSDVDVDMWSLGVISFELLTCSPTVDGAQNSKDIATKRLTKKVPF 246  
246 PSAWSQEWVSLKLEPNPDOR---FQSLSDVQNPFPYNDINMDAVFQKRLIPGIPNKG 303  
247 PKTMDVDARDFIGQLLEKLEKLGNGVDEIKNHFMSIDWDAVAKRTLKEVIVPERIG 306  
RESULT 11  
S19027  
A;Accession: S19027  
A;Gene: Aplysia californica (California sea hare)  
C;Species: Aplysia californica (California sea hare)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 18-Jun-1999  
C;Accession: S19027  
R;Beushausen, S.; Bergold, P.; Sturmer, S.; Elate, A.; Roytenberg, V.; Schwartz, J.H.; Be  
Neuron 1, 853-864, 1988  
A;Title: Two catalytic subunits of cAMP-dependent protein kinase generated by alternative  
A;Reference number: S19027; MUID:90166564; PMID:2483106  
A;Accession: S19027  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-352 <BSU>  
A;Cross-references: EMBL:X63420; NID:95576; PIDN:CAA45014.1; PID:IG5577  
A;Note: the authors translated the codon AAC for residue 29 as Asp, GAC for residue 45 as  
as Glu, CTA for residue 271 as Glu, AAC for residue 285 as Asp, and AAC for residue 288 as  
C;Superfamily: kinase-related transforming protein; protein kinase homology  
C;Keywords: phosphotransferase  
F;42-299/Domain: protein kinase homology <KIN>  
Query Match 24.1%; Score 518; DB 2; Length 352;  
Best Local Similarity 33.6%; Pred. No. 7e-17;  
Matches 109; Conservative 83; Mismatches 102; Indels 30; Gaps 10;  
21 DHPILRAIGKSGFGKVCIVQ---KNDTKMYAMKYNKQKCVNERNEVRNFKELQIMQGLE 79  
42 DDFRIKTLGTSGFRVNLVQHKGESNFYAMKILDKQVVKLQVHTLNEKKILQSN 101  
80 HPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVHKEEIVKLFCICELVMDLYLQ 139  
102 FFLVVKLEYSFKDNLNMYLVLEFVTGEMFSLRRIGRFSRPFYAAQIVLVLEYLHH 161  
140 QRIIHRMDKPNILLDEHGHVHTDANIA-AMPLPRETQITTMAGTKPYMAPENFSSKAG 199  
162 LDIMYRDLKPEKILLDSYGLKVTDFGFAKVKGRT---WTLCGTFEYLAPELILSK---G 216  
200 YSEAVDMWSLGVYATYELLGRPPYHRSSTSKKEIVHTPETTV---VTYPSAWSQEWVSL 256  
217 YNKAVDMWSLGVYATYELLGRPPYHRSSTSKKEIVHTPETTV---ADQPIQIVEKIVSGKVRFSHFDLXDL 270  
257 LKLEPNPDORFQSL---SDVQNPFPYNDINMDAVFQKRLIPGIP-NKGRNLCDPTF 311  
277 LRLNQLQVLTFRFGLNKGNDIKNHFMSIDWDAVAKRTLKEVIVPERIG 327  
312 ELEEMILESKEPLHKKKELAKKEK 335  
328 NFDD---YEEFPL-----RISSTEK 344  
RESULT 12  
T21211  
Hypothetical protein ZK909.2a - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 31-Jan-2000  
C;Accession: T21211; T28100  
R;McLay, K.  
Submitted to the EMBL Data Library, November 1996  
A;Reference number: Z19391  
A;Accession: T21211  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-359 <WIL>  
A;Cross-references: EMBL:Z81511; PIDN:CAB04168.1; GSPDB:GN00019; CESP:ZK909.2a  
A;Experimental source: clone F21F12  
R;White, S.  
Submitted to the EMBL Data Library, November 1996  
A;Reference number: Z20469  
A;Accession: T28100  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-359 <W12>  
A;Cross-references: EMBL:Z82096; PIDN:CAB05034.1; GSPDB:GN00019; CESP:ZK909.2a  
A;Experimental source: clone ZK909  
C;Genetics:  
A;Gene: CESP:ZK909.2a  
A;Map position: 1

A; Introns: 24/1; 44/3; 87/3; 120/3; 190/3; 318/3  
C; Superfamily: Kinase-related transforming protein; protein kinase homology

Query Match 24.0%; Score 517; DB 2; Length 359;  
Best Local Similarity 33.3%; Pred. No. 7.9e-17;  
Matches 110; Conservative 79; Mismatches 119; Indels 22; Gaps 7;

QY 14 ENEDVN---FDHEILRAIGKSGFGKVCIVOKNDTKKMYAMKMKQKCKVERNEVNFK 70  
DB 40 ENPAQNTACLDQFDRIKTLGTSFGFVLMVGHKQSGNYAMKILDKQVKVQLQVHEHTLN 99  
QY 71 ELQIMGLHPEFLVNLWYFQDEDMFMVVDLLGGDLRYHLQONVHFKEETVKLFCEL 130  
DB 100 EKRILOAIDPFVNLWTFSPKNSLYMVFLETSFGGEMFSLRIGRSEPHSRFRAAQI 159  
QY 131 VMALDYLNQRIIHRDMKPDNILLDEGHVHTIDFNIAAMLPEQTQITTMAGTKPYMAPE 190  
DB 160 VLAFYLHSLDLYRDKPENLIDSTGYLKITDFGFAKVGKT--WILCGTPEYLAPE 217  
QY 191 MFSRKGAGYFAVDWMSLGTAYELLRGRPRYHRSSTSSKEIVHTFTV---VTYPS 247  
DB 218 IILSK--GYNKAVDWALGVLYMAAGYPPFF-----ADQIQIYKIVSGKVKFPS 268  
QY 248 ANSQEMVSLIKLLEPNPDQFSQL-----SDVQNFPMNDINWDAVQKELIPGFIEN-K 302  
DB 269 HFSNELKDLKLLQVLDLTKRYGNLKNGVADIKNHWFGSTDMTAYIYKKIEAPFLPKCR 328  
QY 303 GRLCDPTFLEEMILESPLHKKKKRLAK 332  
DB 329 GPGDASNFDDYEEPLRISTGCKAFAE 358

RESULT 13  
S48986  
A; Title: Human protein kinase SCH9 (EC 2.7.1.1) 3 - human  
A; Alternate names: insulin-stimulated protein kinase 1 (PK-1, ISPK1); MAP kinase-activated protein kinase  
A; Species: Homo sapiens (man)  
C; Date: 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 18-Jun-1999  
C; Accession: I38556; I64835  
R; Torbaek, C.; Vik, T.A.; Echwald, S.M.; Webb, G.C.; Wang, J.P.; Yang, P.Y.; Vestergaard, M.; J. Biol. Chem. 266, 351-359, 1994  
A; Title: Cloning of a human insulin-stimulated protein kinase (ISPK-1) gene and analysis of its expression  
A; Reference number: I38556; MUID:95113220; PMID:7813820  
A; Accession: I38556  
A; Status: preliminary; translated from GB/EMBL/DBJ  
A; Molecule type: mRNA  
A; Residues: 1-740 <BU>  
A; Cross-references: EMBL:U08316; NID:9475587; PIDN:AAA81952.1; PID:9475588  
R; Miller, D.E.; Xia, C.H.; Tang, W.; Zhu, A.X.; Jakubowski, M.  
J. Biol. Chem. 266, 351-359, 1994  
A; Title: Human rsk isoforms: cloning and characterization of tissue-specific expression.  
A; Reference number: I51901  
A; Accession: I64835  
A; Status: preliminary; translated from GB/EMBL/DBJ  
A; Molecule type: mRNA  
A; Residues: 2-423, 'L', 425-479, 'N', 481-493, 495-582 <MOL>  
A; Cross-references: GB:L07599; GB:L07601; NID:G401773; PIDN:AA82495.1; PID:G401774  
C; Comment: Although ribosomal protein S6 (see PIR:R3HU6) is phosphorylated by this enzyme  
C; Genetics:  
A; Gene: GDB:RP6K3; RSK; HU-2; RSK2; HU-3  
A; Cross-references: GDB:365648; OMIM:300075  
A; Map position: Xp22.2-Xp22.2  
C; Superfamily: ribosomal protein S6 kinase II; protein kinase homology  
C; Keywords: ATP; monomer; phosphoprotein; phosphotransferase; serine/threonine-specific  
F:66-327/Domain: protein kinase homology <KIN>  
F:74-82/Region: protein kinase ATP-binding motif  
F:420-679/Domain: protein kinase homology <KIN2>  
F:428-436/Region: protein kinase ATP-binding motif

Query Match 23.9%; Score 514.5; DB 2; Length 740;  
Best Local Similarity 35.8%; Pred. No. 2e-16;  
Matches 112; Conservative 65; Mismatches 117; Indels 19; Gaps 7;

QY 111 VDENEDVNFDFEILRAIGKSGFGKVCIVOK---NDTKMYAMKMKQKCKVERNEVNF 67  
DB 55 VKEGHEKADPSQFELLKVLGQSGFGKVFVKKISGDARQLYAMKVLKATLKVDRVET 115  
QY 63 VFKELOIMQGLHPEFLVNLWYFQDEDMFMVVDLLGGDLRYHLQONVHFKEETVKLF 127  
DB 115 KM-ERDILVENHPEFLVNLHYAFQTEGKLYLILDFLGGDLFTRLSKVEMFTEEDVKFYL 174  
QY 128 CELVMALDYLNQRIIHRDMKPDNILLDEGHVHTIDFNIA-AMLPREQTITMAGTKPY 186  
DB 175 AELALALDHLHSLGITYRDLKPDENILDEGHKILDTFGLSKESIDHEKKAYSFGCTVY 234  
QY 187 MAPEMPSSKKGAGYFAVDWMSLGTAYELLRGRPRYHRSSTSSKEIVHTFTVTP 246  
DB 235 MAPEVNNRR---GHTQSDAWMSFGVLMFEMLTGTPF---QKDKRETMTMLKAKLGNP 288  
QY 247 SAMSQEMVSLIKLLEPNPDQFSQL-----LSVQNFPMNDINWDAVQKELIPGFIENK 302  
DB 289 QFLSPAQSLRLMKFKNPANRLGAGPDGVBEIKRHSFSTIDWNKLYRREIHPPEKPAT 348  
QY 303 GR-----LNCODPTF 311  
DB 349 GRPDTFYEDPEF 361

RESULT 14  
S48986  
A; Title: The SCH9 protein kinase mRNA contains a long 5' leader with a small open reading frame  
A; Reference number: S30021; MUID:93182531; PMID:8442384  
A; Accession: S30022  
A; Status: nucleic acid sequence not shown; translation not shown  
A; Molecule type: DNA  
A; Residues: 'M', 1-823 <DIB>  
A; Cross-references: EMBL:X57629; NID:95277; PIDN:CAA40853.1; PID:95279  
A; Note: The nucleotide sequence was submitted to the EMBL Data Library, February 1991  
R; Toda, T.; Cameron, S.; Sass, P.; Wigler, M.  
Genes Dev. 2, 517-527, 1988  
A; Title: SCH9, a gene of *Saccharomyces cerevisiae* that encodes a protein distinct from, I  
Yeast 9, 21-32, 1993  
A; Reference number: A28429; MUID:88255839; PMID:3290050  
A; Accession: A28429  
A; Molecule type: DNA  
A; Residues: 'M', 1-364, 'S', 366-749, 'K', 751-823 <TOD>  
A; Cross-references: EMBL:X12560; NID:G4425; PIDN:CAA31073.1; PID:G4426  
C; Genetics:  
A; Gene: SGD:SCY9  
A; Cross-references: SGD:S0001248; MIPS:YHR205W  
A; Map position: 8R  
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology  
C; Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase  
F:409-670/Domain: protein kinase homology <KIN>  
F:417-425/Region: protein kinase ATP-binding motif

Query Match 23.9%; Score 514.5; DB 2; Length 823;  
Best Local Similarity 31.5%; Pred. No. 2.2e-16;  
Matches 139; Conservative 81; Mismatches 156; Indels 65; Gaps 15;

QY 6 SRKPPVDE--NEDVNF-----DHPEILRAIGKSGFGKVCIVQKNDTKMY 49

```

378 SLKPRVDEVSGLIKWTYKQKKRHYGPQDFVLRLLGKGFQVYQVKKKDTQRIY 437
50 AMKVMKQKVERNEVNFKEIQIM--OGLBHPFLVNLWYSPQDEEDFMVVDLLGG 106
438 AMKVLKVKVVKNEIAHTIGERNILVTTASKSPFTVGLKFSQTFDLYLVTDYMSGG 497
107 DLRLHQQNVHFKEETVKLFCELVAMALDYQONRIIHRDMKPDNILLDEHGHVHTDEN 166
498 ELFWHLQKRGFSDRAKFAIEALVLALEHLHDNDIVYRLKPNILLDANGIALCDFG 557
167 IA-AMLPRETQITTMAGTKPYMAPEMFSRKGAGYSFADWWSLGVYAYELLRGRPYHI 225
558 LSKADLKDRT--NTFCGTTEYLAPELLDDE--TGYTKWVDFWSLGVLIFFEMCCGSPFF- 612
226 RSTSSKEIVHTFTTTPVTP-SAWSEMVSLLKLEPNPDQRFSQLSD---VQNEPYM 281
613 --AENNQMYQKIAFGKVPKPRDVLSQLSGRFSVKGLLNRNPKHRLGAIDDGRELRAHPFF 670
282 NDINWDAVFOKRLIPGFIPI--KGRLLCNDPTE-----ELEEMILSKPLHKKKR 329
671 ADIDWEALKQKIDPPKPHLVSTDTNSDFETTTASTSYMNKHQPMATPL---SPA 727
330 LAKKEDKMRKCDSSQTCILQHLDSVQK-----EFIIIFN-----REKYNRDNFK 373
728 MQAKFAGFTFYDES---AIDSHVANNRKFQNSYEMRPGSFIPGNPNLPDDEDVIDDDGD 784
374 RQPNLALFQTKDPQVNTGQMD 394
785 EDINDGFNQEKNNMNSHSQMD 805

```

```

RESPOT 15
T2122
hybrid protein ZK909.2b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C:Accession: T21212; T28101
R:May, K.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19391
A:Accession: T21212
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-375 <W11>
A:Cross-references: EMBL:Z81511; PIDN: CAB04169.1; GSPDB: GN00019; CESP: ZK909.2b
A:Experimental source: clone F21F12
R:Wolfe, S.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20469
A:Accession: T28101
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-375 <W12>
A:Cross-references: EMBL:Z82096; PIDN: CAB05035.1; GSPDB: GN00019; CESP: ZK909.2b
A:Experimental source: clone ZK909
C:Genetics:
A:Gene: CESP:ZK909.2b
A:Map position: 1
A:Introns: 24/1; 44/3; 87/3; 120/3; 190/3; 318/3
C:Superfamily: Kinase-related transforming protein; protein kinase homology

```

```

Query Match 23.9%; Score 514; DB 2; Length 375;
Best Local Similarity 34.7%; Pred.No. 1.1e-16;
Matches 105; Conservative 75; Mismatches 101; Indels 22; Gaps 7;

QY 14 ENEDVN---FDEFEILRAIGKSGFGKVCIVQKNDTKMYAMKMKQKVERNEVRNFK 70
DB 40 ENPAQNTACLDLDFDKITLGTGSGFGRVLMVKKHQSNGNYAMKILDKQKVVLKQVEHTLN 99
QY 71 ELQIMQGLEHPLVNLWYSPQDEEDFMVVDLLGGDLRYHLQQNVHFKETVKLFICEL 130
DB 100 EKRLQAIQDFPFLVNNVTFKNSNLYMVLEFTSGGEMFSLRLRIGRFSEPHSRFYAAQI 159

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QY 131 VMALDYQONRIIHRDMKPDNILLDEHGHVHTDENIAAMLPRETQITTMAGTKPYMAPE 190
DB 160 VLAPEYVLSLDLYRDLKPNILLDSTGYLKITDFGFAKRVKGR--WTLCGTPEYLAPE 217
QY 191 MFSRKGAGYSFADWWSLGVYAYELLRGRPYHRSSTSSKEIVHTFTTV---VTYPS 247
DB 218 IILSK--GYNKAVDWMALGVLIYEMAAGYPPFF-----ADQPIQIYEKIVSGKVKFPFS 268
QY 248 AWSQEMVSLLKLEPNPDQRFSQL---SDVQNFPMNDINWDVAFQKRLIPGFIPIPKG 303
DB 269 HFSNELKDLLNLLQVLDLTKRYGNLKNGVADIKNHNKFWGSTDNIAIYQKILTPSPF-SKG 327
QY 304 RLN 305
DB 328 ESN 330

```

Search completed: May 26, 2004, 20:20:20  
Job time : 21 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 26, 2004, 20:08:13 ; Search time 59 Seconds  
(without alignments)  
1949.099 Million cell updates/sec

Title: US-10-620-845-9

Perfect score: 2151

Sequence: 1 MGANTSRKPPVDFENEDVNF.....VTNGQMDTGLSETQTSKVS 407

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Sequenced: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Date: A\_Geneseq\_29Jan04:\*

- 1: Genesep1980s:\*
- 2: Genesep1990s:\*
- 3: Genesep2000s:\*
- 4: Genesep2001s:\*
- 5: Genesep2002s:\*
- 6: Genesep2003as:\*
- 7: Genesep2003bs:\*
- 8: Genesep2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Score	Query Match	Length	DB ID	Description
1	2151	100.0	407	5	AAE14260 Novel hum
2	2060	95.8	396	4	AAE14260 Human pro
3	2060	95.8	396	5	AAE14261 Novel hum
4	2060	95.8	396	5	AAE21725 Human PKI
5	2054	95.5	396	5	AAE50334 Human 149
6	2047	95.2	396	6	ABG70700 Human ser
7	2047	95.2	396	6	ABU62276 Human kin
8	1513.5	70.4	327	4	AAU03504 Human pro
9	1430.5	66.5	404	6	ABU62277 Mouse ser
10	1423.5	66.2	403	6	ABU62278 Human ser
11	1423.5	66.2	414	4	AAE56500 Novel pro
12	1423.5	66.2	414	5	ABP43807 Serine/th
13	1423.5	66.2	414	5	AAO17710 Human ser
14	1423.5	66.2	414	6	ABR58617 Human can
15	1423.5	66.2	414	7	ABR38375 Human pro
16	1333.5	62.0	419	4	AAE65599 Novel pro
17	1333.5	62.0	488	5	AAO17709 Murine se
18	1331	61.9	485	5	AAE24141 Human kin
19	1329.5	61.8	425	4	AAW40592 Human pol
20	1328.5	61.8	384	6	ABU62279 Mouse ser
21	1323.5	61.5	419	4	AAE38806 Human pol
22	1310.5	60.9	488	6	ABO14992 Human NOV
23	1294.5	60.2	399	5	ABR84300 Murine se
24	1294	60.2	713	5	ABR06090 Human NS
25	1272.5	59.2	375	4	AAE04371 Human kin

## ALIGNMENTS

RESULT 1  
AAE14260  
ID AAE14260 standard; protein; 407 AA.

XX AAE14260;

XX 07-MAR-2002 (first entry)

XX Novel human protein (NHP) kinase #3.

XX Novel human protein; NHP; gene therapy; diagnosis; drug screening;

XX gene expression; breast cancer; prostate cancer; nutraceutical; cosmetic; medical disorder; mental; biological; physiological; chemotherapeutic.

XX Homo sapiens.

XX WO20018:557-A2.

XX 01-NOV-2001.

XX 24-APR-2001; 2001WO-US013149.

XX 25-APR-2000; 2000US-0199499P.

XX 01-MAY-2000; 2000US-0201227P.

XX (LEXI-) LEXICON GENETICS INC.

XX Hu Y, Nepomichy B, Wang X, Donoho G, Scoville J, Walke DW;

XX WPI: 2002-034442/04.

XX N-PSDB; AAD23678.

XX New nucleic acid molecules encoding new human proteins, useful in diagnosis, drug screening, clinical trial monitoring, treatment of physiological disorders, and cosmetic or nutraceutical applications.

XX Claim 5; Page 41-42; 44pp; English.

XX The invention relates to novel human protein (NHP) kinases and their corresponding cDNA molecules. NHP kinase and its DNA are useful as reagents in assays for screening compounds that can be used as pharmacological reagents useful in the therapeutic treatment of mental, biological and medical disorders, and also as chemotherapeutic agents useful in the treatment of breast cancer and prostate cancer. NHP DNA is useful for diagnosis, drug screening, clinical trial monitoring, the treatment of physiological disorders or diseases, and cosmetic and nutraceutical applications. NHP DNA is also useful for the identification of coding sequence and the mapping of a unique gene to a particular

26	1194.5	55.5	444	6	AAE37974	Aae37974 Human kin
27	1151	55.4	364	5	AAO17708	Aao17708 Human ser
28	1186.5	55.2	364	4	AAU29309	Aau29309 Human PRO
29	1186.5	55.2	364	6	ABU58685	Abu58685 Human PRO
30	1186.5	55.2	364	6	ABU82333	Abu82333 Novel hum
31	1186.5	55.2	364	6	ABU84548	Abu84548 Human sec
32	1186.5	55.2	364	6	ABR66422	AbR66422 Human sec
33	1186.5	55.2	364	6	ABR65812	AbR65812 Human sec
34	1186.5	55.2	364	6	ABU99752	Abu99752 Human sec
35	1186.5	55.2	364	6	ABU82991	Abu82991 Human PRO
36	1186.5	55.2	364	6	ABU90112	Abu90112 Novel hum
37	1186.5	55.2	364	6	ABR68361	AbR68361 Human sec
38	1186.5	55.2	364	6	ABU96414	Abu96414 Novel hum
39	1186.5	55.2	364	6	ABU92845	Abu92845 Human sec
40	1186.5	55.2	364	6	ABO08922	ABO08922 Human sec
41	1186.5	55.2	364	6	ABO02974	ABO02974 Human sec
42	1186.5	55.2	364	6	ABR75128	AbR75128 Human sec
43	1186.5	55.2	364	6	ABR94890	AbR94890 Human sec
44	1186.5	55.2	364	6	ABR5863	AbR5863 Human PRO
45	1186.5	55.2	364	6	ABU99023	Abu99023 Novel hum

CC chromosome. NHP DNA is further useful as hybridisation probes for  
CC screening libraries and assessing gene expression patterns, and also for  
CC the detection of mutant NHPs or inappropriately expressed NHPs for  
CC disease diagnosis. NHP DNA is also useful in gene therapy. The present  
CC sequence is novel human protein (NHP) kinase which is similar to  
CC serine/threonine protein kinases, ribosomal protein kinases and cAMP-  
CC dependent kinases related to the invention

XX SQ Sequence 407 AA;

Query Match 100.0%; Score 2151; DB 5; Length 407;  
Best Local Similarity 100.0%; Pred. No. 8e-196;  
Matches 407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGANTSRRPPVFDENEDVNFDFHLLRAIGKSGFKVICIVQKNDTKKMYAMKYNKQKCV 60  
D 1 MGANTSRRPPVFDENEDVNFDFHLLRAIGKSGFKVICIVQKNDTKKMYAMKYNKQKCV 60  
QY 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVHPE 120  
D 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVHPE 120  
QY 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEGHVHITDFNTAAMPLPRETQITTM 180  
D 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEGHVHITDFNTAAMPLPRETQITTM 180  
QY 181 AGTGYMAPEMFSSRKAGYGFVDMWSLGVYAVELLGRPPYHRSSTSSKEIVHTPET 240  
D 181 AGTGYMAPEMFSSRKAGYGFVDMWSLGVYAVELLGRPPYHRSSTSSKEIVHTPET 240  
QY 241 TVVTYPSAWSQEMVSLKLLKLEPNDFQSFQSDVQNFPPYNDINWDAVFQKRLIPGIP 300  
D 241 TVVTYPSAWSQEMVSLKLLKLEPNDFQSFQSDVQNFPPYNDINWDAVFQKRLIPGIP 300  
QY 301 NKGRLNCDPTFELEEMILESPLHKKKRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 360  
D 301 NKGRLNCDPTFELEEMILESPLHKKKRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 360  
QY 361 IFNREKVNDRDNKROPNLALEQTKDPQVINGQMDTGLSETFQTSKVS 407  
D 361 IFNREKVNDRDNKROPNLALEQTKDPQVINGQMDTGLSETFQTSKVS 407

RESULT 2

AAB85491 standard; protein; 396 AA.

AAB85491;

25-SEP-2001 (first entry)

Human protein kinase SGK177.

Protein kinase; enzyme; cytostatic; neurotropic; neuroprotective; human;  
antiparkinsonian; virucide; antibacterial; antifungal; antimigraine;  
analgesic; hypotensive; hypertensive; immunosuppressive; antiallergic;  
antipsoriatic; antirheumatic; antiarthritic; ophthalmological; anorectic;  
osteopathic; thrombolytic; antiarteriosclerotic; antiasthmatic;  
vasotrophic; antidiabetic; gene therapy.

Homo sapiens.

WC200155356-A2.

02-AUG-2001.

25-JAN-2001; 2001WO-US002337.

25-JAN-2000; 2000US-0178078P.

31-JAN-2000; 2000US-0179364P.

17-FEB-2000; 2000US-0183173P.

17-MAR-2000; 2000US-0190162P.

29-MAR-2000; 2000US-0193404P.

13-NOV-2000; 2000US-0247013P.

(SUGEN-) SUGEN INC.

Plowman G, Whyte D, Manning G, Sudarsanam S, Martinez R;

WPI; 2001-476202/51.

N-PSDB; AAB46891.

Kinase polypeptides useful for treating cancers, Alzheimer's disease,  
viral infections, diabetes, obesity, organ transplant rejection and  
rheumatoid arthritis.

Claim 7; Page 214; 219pp; English.

The invention provides human protein kinases and protein kinase-like  
enzymes and polynucleotides encoding the polypeptides. The kinase  
polypeptides and their modulators are useful for treating a disease or  
disorder such as cancer, immune-related diseases, cardiovascular disease,  
brain or neuronal-associated disease and metabolic disorders, including  
cancers of tissues, cancers of hematopoietic origin, diseases of the  
central nervous system, diseases of the peripheral nervous system.  
Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic  
lateral sclerosis, viral infections, infections caused by prions,  
bacteria and fungi, ocular diseases, migraines, pain, sexual dysfunction,  
mood disorders, attention disorders, neurological disorders, dyskinesias,  
hypertension, psychotic disorders, neurodegenerative disorders, chronic  
metabolic disorders, and organ transplant rejection. They are also useful  
for treating rhinitis, autoimmunity, atherosclerosis, psoriasis,  
osteoarthritis, asthma, chronic inflammatory arthritis, metabolic disorders  
inflammatory bowel disease, rheumatoid arthritis, metabolic disorders  
such as diabetes, obesity, cardiovascular diseases such as reperfusion  
injury, coronary thrombosis, clotting disorders and atherosclerosis,  
ocular diseases such as glaucoma, retinopathy and macular degeneration,  
psychiatric and neurological disorders such as anxiety, schizophrenia,  
dementia, manic depression, etc. The polynucleotides are useful in gene  
therapy techniques to treat the above mentioned disorders. Sequences  
AAB85491-85522 represent the human protein kinases of the invention

Sequence 396 AA;

Query Match 95.8%; Score 2060; DB 4; Length 396;  
Best Local Similarity 99.2%; Pred. No. 3.6e-187;  
Matches 389; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGANTSRRPPVFDENEDVNFDFHLLRAIGKSGFKVICIVQKNDTKKMYAMKYNKQKCV 60

D 1 MGANTSRRPPVFDENEDVNFDFHLLRAIGKSGFKVICIVQKNDTKKMYAMKYNKQKCV 60

QY 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVHPE 120

D 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVHPE 120

QY 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEGHVHITDFNTAAMPLPRETQITTM 180

D 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEGHVHITDFNTAAMPLPRETQITTM 180

QY 181 AGTGYMAPEMFSSRKAGYGFVDMWSLGVYAVELLGRPPYHRSSTSSKEIVHTPET 240

D 181 AGTGYMAPEMFSSRKAGYGFVDMWSLGVYAVELLGRPPYHRSSTSSKEIVHTPET 240

QY 241 TVVTYPSAWSQEMVSLKLLKLEPNDFQSFQSDVQNFPPYNDINWDAVFQKRLIPGIP 300

D 241 TVVTYPSAWSQEMVSLKLLKLEPNDFQSFQSDVQNFPPYNDINWDAVFQKRLIPGIP 300

QY 301 NKGRLNCDPTFELEEMILESPLHKKKRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 360

D 301 NKGRLNCDPTFELEEMILESPLHKKKRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 360

QY 361 IFNREKVNDRDNKROPNLALEQTKDPQVINGQ 392

D 361 IFNREKVNDRDNKROPNLALEQTKDPQVINGQ 392

RESULT 3  
AAE14261  
ID AAE14261 standard; protein; 396 AA.  
XX  
AC AAE14261;  
XX  
DT 07-MAR-2002 (first entry)  
XX  
DE Novel human protein (NHP) kinase #4.  
XX  
KW Novel human protein; NHP; gene therapy; diagnosis; drug screening;  
KW gene expression; breast cancer; prostate cancer; nutraceutical; cosmetic;  
KW medical disorder; mental; biological; physiological; chemotherapeutic.  
XX  
OS Homo sapiens.  
XX  
PN WO200181557-A2.  
XX  
PD 01-NOV-2001.  
XX  
PF 24-APR-2001; 2001WO-US013149.  
XX  
PR 25-APR-2000; 2000US-0199499P.  
XX  
PR 01-MAY-2000; 2000US-0201227P.  
XX  
PA (LEXI-) LEXICON GENETICS INC.  
XX  
PI Hu Y, Nepomnichy B, Wang X, Donoho G, Scoville J, Walke DW;  
PI DR MWPI; 2002-034442/04.  
XX  
PI DR N-PSDB; AAD23679.  
XX  
PI New nucleic acid molecules encoding new human proteins, useful in  
PI diagnosis, drug screening, clinical trial monitoring, treatment of  
PI physiological disorders, and cosmetic or nutraceutical applications.  
XX  
PS Claim 7; Page 43; 44pp; English.  
XX  
CC The invention relates to novel human protein (NHP) kinases and their  
CC corresponding cDNA molecules. NHP kinase and its DNA are useful as  
CC reagents in assays for screening compounds that can be used as  
CC pharmaceutical reagents useful in the therapeutic treatment of mental,  
CC biological and medical disorders, and also as chemotherapeutic agents  
CC useful in the treatment of breast cancer and prostate cancer. NHP DNA is  
CC useful for diagnosis, drug screening, clinical trial monitoring, the  
CC treatment of physiological disorders or diseases, and cosmetic and  
CC nutraceutical applications. NHP DNA is also useful for the identification  
CC of coding sequence and the mapping of a unique gene to a particular  
CC chromosome. NHP DNA is further useful as hybridisation probes for  
CC screening libraries and assessing gene expression patterns, and also for  
CC the detection of mutant NHPs or inappropriately expressed NHPs for  
CC disease diagnosis. NHP DNA is also useful in gene therapy. The present  
CC sequence is novel human protein (NHP) kinase which is similar to  
CC serine/threonine protein kinases, ribosomal protein kinases and cAMP-  
CC dependent kinases related to the invention  
XX  
SQ Sequence 396 AA;  
Query Match 95.8%; Score 2060; DB 5; Length 396;  
Best Local Similarity 99.2%; Pred. No. 3.6e-187;  
Matches 389; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MGANTSRRPPVFDENEDYVDFHFEILRAIGKSGFKVCIVKNDPKMYAMKYNKQKCV 60  
DB 1 MGANTSRRPPVFDENEDYVDFHFEILRAIGKSGFKVCIVKNDPKMYAMKYNKQKCV 60  
QY 61 ERNEVRNVFKELQINQGLEHPLVNLWTSFQDEEDMFVMDLLGLDLYHLQNVHFEK 120  
DB 61 ERNEVRNVFKELQINQGLEHPLVNLWTSFQDEEDMFVMDLLGLDLYHLQNVHFEK 120  
QY 121 ETVKLFICELVMDLYLQNRRIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180

Db 121 ETVKLFICELVMDLYLQNRRIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180  
QY 181 AGTKPYMAPEMFSSRRKAGYSFAVDWWSLGVTAAYELLGRPRPYHRSSTSSKEIVHFTET 240  
Db 181 AGTKPYMAPEMFSSRRKAGYSFAVDWWSLGVTAAYELLGRPRPYHRSSTSSKEIVHFTET 240  
QY 241 TVVTYPSAQSQENWSLLKKLEENPDORPSQSDVQNFYPMNDINWDVAFQKELIPGPIP 300  
Db 241 TVVTYPSAQSQENWSLLKKLEENPDORPSQSDVQNFYPMNDINWDVAFQKELIPGPIP 300  
QY 301 NKGRINCDPTFELEEMILSKPLHKKKRLAKKEDMRKCDSSQTCILQEHLSVQKEFI 360  
Db 301 NKGRINCDPTFELEEMILSKPLHKKKRLAKKEDMRKCDSSQTCILQEHLSVQKEFI 360  
QY 361 IFNREKVRNDRFNKRQPNLALEQTKDPQVINGQ 392  
Db 361 IFNREKVRNDRFNKRQPNLALEQTKDPQGEDGQ 392  
RESULT 4  
AAE21725  
ID AAE21725 standard; protein; 396 AA.  
XX  
AC AAE21725;  
XX  
DT 16-JUL-2002 (first entry)  
XX  
DE Human PKIN-20 protein.  
XX  
KW Human; kinase; enzyme; PKIN-20 protein; immune system disorder; anaemia;  
KW acquired immune deficiency syndrome; thymic hypoplasia; Crohn's disease;  
KW asthma; neurological disorder; epilepsy; Charcot-Marie-Tooth disease;  
KW AIDS; seizures; cell proliferative disorder; cancer; adenocarcinoma;  
KW leukaemia; lymphoma; melanoma; sarcoma; developmental disorder;  
KW Down's syndrome; gene therapy; protein therapy; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PH Key Location/Qualifiers  
XX Domain 13..300 /note= "Protein kinase domain"  
XX Domain 23..300 /note= "Protein kinase domain"  
XX Domain 23..281 /note= "Eukaryotic protein kinase domain"  
XX Domain 25..270 /note= "Protein kinase domain"  
XX Domain 25..268 /note= "Protein kinase domain"  
XX WO200218557-A2.  
XX 07-MAR-2002.  
XX 31-AUG-2001; 2001WO-US027219.  
XX 31-AUG-2000; 2000US-0229873P.  
XX 08-SEP-2000; 2000US-0231357P.  
XX 14-SEP-2000; 2000US-0232654P.  
XX 22-SEP-2000; 2000US-0234902P.  
XX 29-SEP-2000; 2000US-0236499P.  
XX 06-OCT-2000; 2000US-0238389P.  
XX 13-OCT-2000; 2000US-0240542P.  
XX (INCY-) INCYTE GENOMICS INC.  
XX Bandman O, Nguyen DB, Hafalia AJA, Yao MG, Gandhi AR;  
XX Gururajan R, Ding L, Patterson C, Yue H, Baughn MR, Tribouley CM;  
XX Thornton M, Elliott VS, Lu Y, Ison CH, Au-Young J, Tang Y;  
XX Azimzai Y, Burrill JD, Marcus GA, Zingler KA, Lu DAM, Lal PG;  
XX Rankumar J, Warren BA, Kearney L, Policky JL, Thangavelu K;  
XX Burford N;





CC and/or differentiation disorders. A claimed method of treating cancer or  
CC a cellular proliferation and/or differentiation disorder, especially  
CC lung, colon, brain and breast cancer, uses a small molecule, peptide,  
CC phosphopeptide, anti-14911 antibody, a 14911 polypeptide or its variant.  
CC Other disorders that may be diagnosed/treated include those associated  
CC with bone metabolism, autoimmune diseases, cardiovascular disorders,  
CC liver disorders, viral diseases, pain and metabolic disorders  
XX  
SQ Sequence 396 AA;  
  
Query Match 95.5%; Score 2054; DB 5; Length 396;  
Best Local Similarity 99.0%; Pred. No. 1.3e-186;  
Matches 388; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 MGANTSRRKPPVFDENEDVNFHPELRAIGKSGFKVCIQVQNDTKKQYAMKYNKQKCV 60  
Db |||||  
Qy 1 MGANTSRRKPPVFDENEDVNFHPELRAIGKSGFKVCIQVQNDTKKQYAMKYNKQKCV 60  
Db |||||  
Qy 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDMFVMDLLGGDLRYHLQNVHPKE 120  
Db |||||  
Qy 61 ERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDEEDMFVMDLLGGDLRYHLQNVHPKE 120  
Db |||||  
Qy 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180  
Db |||||  
Qy 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180  
Db |||||  
Qy 181 AGTKPYMAPEMFSSKRGAGYSFADVWSLGVTVAYELLGRRPYHRSSTSSKEIVHTPET 240  
Db |||||  
Qy 181 AGTKPYMAPEMFSSKRGAGYSFADVWSLGVTVAYELLGRRPYHRSSTSSKEIVHTPET 240  
Db |||||  
Qy 241 TVVTYPSAWSQEMWSLLKLEPNPDQRFSQLSDVQNFPPYMDINWDVAFQKRLIPGP 300  
Db |||||  
Qy 241 TVVTYPSAWSQEMWSLLKLEPNPDQRFSQLSDVQNFPPYMDINWDVAFQKRLIPGP 300  
Db |||||  
Qy 301 NKGRNLCDPTFLEEMILESPLHKKKXKLAKEKDMKCDSSQTCCLQEHLDLSVQKEFI 360  
Db |||||  
Qy 301 NKGRNLCDPTFLEEMILESPLHKKKXKLAKEKDMKCDSSQTCCLQEHLDLSVQKEFI 360  
Db |||||  
Qy 361 IFNREKVRNDFNKRQPNLALEOTKDPQVINGQ 392  
Db |||||  
Qy 361 IFNREKVRNDFNKRQPNLALEOTKDPQGEDGQ 392  
Db |||||  
RESULT 6  
ABG70700  
ID: ABG70700 standard; protein; 396 AA.  
XX  
XX ABG70700;  
XX  
XX 17-JAN-2003 (first entry)  
XX  
XX Human serine/threonine protein kinase-like kinase.  
XX  
XX Human; kinase; serine/threonine kinase; immune response; transgenic;  
XX enzyme.  
XX  
XX Homo sapiens.  
XX  
XX Key  
XX Location/Qualifiers  
XX Modified-site 2..7 /label= N\_myristoylation\_site  
XX Modified-site 4..7 /label= N\_glycosylation\_site  
XX Modified-site 5..7 /label= Protein\_kinase\_C\_phosphorylation\_site  
XX Modified-site 6..8 /label= Protein\_kinase\_C\_phosphorylation\_site  
XX Binding-site 29..52 /label= Protein\_kinase\_ATP-binding\_region  
XX Modified-site 33..36 /label= Casein\_kinase\_II\_phosphorylation\_site  
XX Modified-site 43..46 /label= N\_glycosylation\_site  
XX

FT Modified-site 45..47 /label= Protein\_kinase\_C\_phosphorylation\_site  
FT Modified-site 89..92 /label= Casein\_kinase\_II\_phosphorylation\_site  
FT Modified-site 122..124 /label= Protein\_kinase\_C\_phosphorylation\_site  
FT Active-site 142..154 /label= Serine/threonine\_protein\_kinase\_active\_site  
FT Modified-site 193..195 /label= Protein\_kinase\_C\_phosphorylation\_site  
FT Modified-site 194..196 /label= Protein\_kinase\_C\_phosphorylation\_site  
FT Modified-site 197..202 /label= N\_myristoylation\_site  
FT Modified-site 212..215 /label= Casein\_kinase\_II\_phosphorylation\_site  
FT Modified-site 218..221 /label= Amidation\_site  
FT Modified-site 230..233 /label= Casein\_kinase\_II\_phosphorylation\_site  
FT Modified-site 391..396 /label= N\_myristoylation\_site  
XX  
XX US2002127683-A1.  
PD 12-SEP-2002.  
XX  
XX 09-MAR-2001; 2001US-00801876.  
XX  
XX 09-MAR-2001; 2001US-00801876.  
XX  
XX (YEJ/J) YE J.  
XX (YANC/) YAN C.  
XX (DFRA/) DI FRANCESCO V.  
XX (BEAS/) BEASLEY E M.  
XX  
XX Ye J, Yan C, Di Francesco V, Beasley EM;  
XX WPI; 2003-028938/02.  
XX N-PSDB; ABS55499, ABS55500.  
XX  
XX Novel isolated human kinase peptide useful for treating disorder  
XX characterized by absence of, in appropriate or unwanted expression of the  
XX kinase protein, and as immunogens to raise antibodies.  
XX  
XX Claim 1; Fig 2; 174pp; English.  
XX  
XX The present invention relates to the isolation of a human kinase and the  
XX polynucleotide sequences encoding it. The human kinase of the invention  
XX is related to the serine/threonine kinase subfamily. The gene encoding  
XX the human kinase is located on chromosome 5. The polypeptide and  
XX polynucleotide sequences of the invention are useful for treating a  
XX disease or condition mediated by a human kinase. Both the polypeptide and  
XX polynucleotide sequences are useful as models for the development of  
XX human therapeutics, for identifying therapeutic proteins, as targets for  
XX development of human therapeutic agents, and as query sequences to  
XX perform a search against sequence data bases to identify other family  
XX members of related sequences. The polypeptide is useful to raise  
XX antibodies or to elicit another immune response, as a reagent in assays  
XX designed to quantitatively determine levels of the protein in biological  
XX fluids, as markers for tissues in which the corresponding protein is  
XX preferentially expressed, in drug screening assays, in cell-based or cell  
XX -free systems, to identify compounds that modulate kinase activity of the  
XX protein in its natural state, or an altered form that causes the specific  
XX disease or pathology associated with the kinase, to screen a compound for  
XX the ability to stimulate or inhibit interaction between the kinase  
XX protein and a molecule that normally interacts with the kinase protein,  
XX and in pharmacogenomic analysis. The polynucleotide is useful for  
XX monitoring the effectiveness of modulating compounds on the expression or  
XX activity of the human kinase gene in clinical trials or in a treatment  
XX regimen, in diagnostic assays for qualitative changes in a human kinase  
XX nucleic acid that leads to a pathology, for testing an individual for a  
XX genotype that while not necessarily causing a disease, nevertheless  
XX

CC affects the treatment modality, as antisense constructs to control human  
 CC kinase gene expression in cells, tissues and organisms, for gene therapy  
 CC in patients containing cells that are aberrant in human kinase gene  
 CC expression, and to produce transgenic animals. The present sequence  
 CC represents a human kinase related to the serine/threonine protein kinase  
 CC subfamily  
 XX  
 SQ Sequence 396 AA;  
 Query Match 95.2%; Score 2047; DB 6; Length 396;  
 Best Local Similarity 98.7%; Pred. No. 6.2e-186;  
 Matches 387; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MGANTSRKPPVFEDENEDVDFEILRAIGKSGFGKVCIVQKNDTKMAYAMKYNKQCV 60  
 DB 1 MGANTSRKPPVFEDENEDVDFEILRAIGKSGFGKVCIVQKNDTKMAYAMKYNKQCV 60  
 QY 61 ERNEVRNVFKELQIMOGLEHPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQNVHFKE 120  
 DB 61 ERNEVRNVFKELQIMOGLEHPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQNVHFKE 120  
 QY 121 ETVKLFICELVMDLYLQNRQIIRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180  
 DB 121 ETVKLFICELVMDLYLQNRQIIRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180  
 QY 181 AGTKPYMAPEMFSSRKAGYSFAVDWMSLGVATYELLGRPPYHRSSTSSKEIVHVFET 240  
 DB 181 AGTKPYMAPEMFSSRKAGYSFAVDWMSLGVATYELLGRPPYHRSSTSSKEIVHVFET 240  
 QY 241 TVVTYPSANSQEMVSLIKLLEPNDFQSLSDVQNFYPMNDINMDAVFKRLIPGIP 300  
 DB 241 TVVTYPSANSQEMVSLIKLLEPNDFQSLSDVQNFYPMNDINMDAVFKRLIPGIP 300  
 QY 301 NKGRNLCDPTFEEEMILESPLHKKKRLAKKEKDMRKCDSSQTCLLQEHLSVQKEFI 360  
 DB 301 NKGRNLCDPTFEEEMILESPLHKKKRLAKKEKDMRKCDSSQTCLLQEHLSVQKEFI 360  
 QY 361 IFNREKVNDRFNKQPNLALEQTKDPQVINGQ 392  
 DB 361 IFNREKVNDRFNKQPNLALEQTKDPQGEDGQ 392  
 RESULT 7  
 AAU03504  
 ABU62276 standard; protein; 396 AA.  
 ABU62276;  
 01-SEP-2003 (first entry)  
 Human kinase.  
 Human; enzyme; kinase; gene therapy; cancer; inflammation; psoriasis;  
 arteriosclerosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003027307-A1.  
 XX  
 PD 06-FEB-2003.  
 XX  
 XX 26-SEP-2002; 2002US-00254869.  
 FF  
 XX 09-MAR-2001; 2001US-00801876.  
 PR  
 XX (APPL-) APPLERA CORP.  
 PA  
 XX Ye J, Yan C, Di Francesco V, Beasley EM;  
 PI  
 XX WPI; 2003-492035/58.  
 DR  
 DR N-PSDB; ACA62840, ACA62841.  
 XX  
 XX New isolated human kinase proteins, useful for treating disorders  
 PT

PT mediated by kinase pathway (e.g. cancers, inflammations, arteriosclerosis  
 PT or psoriasis), or for development of human therapeutics and diagnostic  
 PT compositions.  
 XX  
 XX Claim 1; Fig 2A; 185pp; English.  
 CC The invention relates to a new isolated human kinase peptide. The human  
 CC kinase peptide and nucleic acid molecules are useful in the development  
 CC of human therapeutics and diagnostic compositions. The peptides are  
 CC useful for treating disorders (e.g. cancers, inflammations,  
 CC arteriosclerosis or psoriasis) characterised by an absence of,  
 CC inappropriate, or unwanted expression of the kinase protein. These  
 CC molecules are particularly useful as models for developing human  
 CC therapeutic targets, identifying therapeutic proteins, or serving as  
 CC targets for the development of human therapeutic agents that modulate  
 CC kinase activity in cells and tissues that express the kinase. The  
 CC peptides are also useful for raising antibodies or eliciting an immune  
 CC response; as a reagent (including the labelled reagent) in assays  
 CC designed to quantitatively determine levels of the protein (or its  
 CC binding partner or ligand) in biological fluids; or as markers for  
 CC tissues in which the corresponding protein is preferentially expressed.  
 CC The agents identified are useful for treating a subject with a disorder  
 CC mediated by kinase pathway. The present sequence represents the amino  
 CC acid sequence of a human kinase  
 XX  
 SQ Sequence 396 AA;  
 Query Match 95.2%; Score 2047; DB 6; Length 396;  
 Best Local Similarity 98.7%; Pred. No. 6.2e-186;  
 Matches 387; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MGANTSRKPPVFEDENEDVDFEILRAIGKSGFGKVCIVQKNDTKMAYAMKYNKQCV 60  
 DB 1 MGANTSRKPPVFEDENEDVDFEILRAIGKSGFGKVCIVQKNDTKMAYAMKYNKQCV 60  
 QY 61 ERNEVRNVFKELQIMOGLEHPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQNVHFKE 120  
 DB 61 ERNEVRNVFKELQIMOGLEHPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQNVHFKE 120  
 QY 121 ETVKLFICELVMDLYLQNRQIIRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180  
 DB 121 ETVKLFICELVMDLYLQNRQIIRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180  
 QY 181 AGTKPYMAPEMFSSRKAGYSFAVDWMSLGVATYELLGRPPYHRSSTSSKEIVHVFET 240  
 DB 181 AGTKPYMAPEMFSSRKAGYSFAVDWMSLGVATYELLGRPPYHRSSTSSKEIVHVFET 240  
 QY 241 TVVTYPSANSQEMVSLIKLLEPNDFQSLSDVQNFYPMNDINMDAVFKRLIPGIP 300  
 DB 241 TVVTYPSANSQEMVSLIKLLEPNDFQSLSDVQNFYPMNDINMDAVFKRLIPGIP 300  
 QY 301 NKGRNLCDPTFEEEMILESPLHKKKRLAKKEKDMRKCDSSQTCLLQEHLSVQKEFI 360  
 DB 301 NKGRNLCDPTFEEEMILESPLHKKKRLAKKEKDMRKCDSSQTCLLQEHLSVQKEFI 360  
 QY 361 IFNREKVNDRFNKQPNLALEQTKDPQVINGQ 392  
 DB 361 IFNREKVNDRFNKQPNLALEQTKDPQGEDGQ 392  
 RESULT 8  
 AAU03504  
 ID AAU03504 standard; protein; 327 AA.  
 XX  
 AC AAU03504;  
 AC  
 XX 12-SEP-2001 (first entry)  
 DT  
 XX Human protein kinase #4.  
 DE  
 XX Human; protein kinase; PTK; STK; cancer; cardiovascular disease;  
 XX metabolic disorder; immune related disease; neurological disorder;  
 KW neurodegenerative disorder; inflammatory disorder; infectious disease;  
 KW

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reproductive disorder.  
Homo sapiens.  
WO200138503-A2.  
31-MAY-2001.  
22-NOV-2000; 2000WO-US032085.  
24-NOV-1999; 99US-0167482P.  
(SUGE-) SUGEN INC.  
Florman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;  
Flanagan P, Clary D;  
WPI; 2001-343950/36.  
N-PSDB; AAS06704.  
Nucleic acids encoding human kinase polypeptides, useful for preventing  
diagnosing and/or treating e.g. cancer, immune, cardiovascular and  
neural-associated diseases, and microbial infections.  
Claim 7; Fig 2; 433pp; English.  
AAU03501-AAU03557 represent novel human protein kinases #1-57. The novel  
protein kinases have been identified as members of the tyrosine or  
serine/threonine kinase (PTK and STK) families. The polynucleotides  
encoding protein kinases and the polypeptides may be used in the  
prevention, diagnosis and treatment of diseases associated with  
inappropriate kinase expression. For example, they may be used to treat  
cancers (especially cancers of hematopoietic origin), cardiovascular  
disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),  
immune related diseases (e.g. rheumatoid arthritis), neurological  
disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.  
Parkinson's disease), inflammatory disorders (e.g. asthma), infectious  
disease (e.g. HIV) and reproductive disorders (e.g. infertility).  
Additionally, polynucleotides encoding protein kinases may be used for  
gene therapy and as DNA probes in diagnostic assays. The protein kinase  
polypeptides may be used as antigens in the production of antibodies  
against the protein kinases and in assays to identify modulators of  
protein kinase expression and activity

Query Match 70.4%; Score 1513.5; DB 4; Length 327;  
Best Local Similarity 87.6%; Pred. No. 2.9e-135; Mismatches 19; Gaps 4;  
Matches 297; Conservative 5; Indels 19; Gaps 4;  
1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKV 60  
1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKV 60  
61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFK 120  
61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFK 120  
121 ETVKLFICELVWALDYLNQRIIHRDMKPDNLLDEHGHVHTTDFNIAAMLPRETQITM 180  
121 ETVKLFICELVWALDYLNQRIIHRDMKPDNLLDEHGHVHTTDFNIAAMLPRETQITM 180  
181 AGTKPMAEMSSRKAGYSAVDWWSLGVATYELLGRREPHYHRSSTSSKEIVHTFET 240  
181 AGTKPMAEMSSRKAGYSAVDWWSLGVATYELLGRREPHYHRSSTSSKEIVHTFET 240  
241 TVVTYPSAWSQEMVSLKKLLE-----PNPDQFQSLSVQ-----NPPYNDINWDVAFQKR 293  
241 TVVTYPSAWSQEMVSLKKVRRKTACPNVETKGRSLGSLSEVSIQY-----WGHQLSSL 295  
294 LIPGFTPNKGRINCDDTTFEELSEMLSKPLHKKKRLAK 332  
296 -----QKGRINCDDTTFEELSEMLSKPLHKKKRLAK 327

Query Match 66.5%; Score 1430.5; DB 6; Length 404;  
Best Local Similarity 68.1%; Pred. No. 3.2e-127;  
Matches 280; Conservative 43; Mismatches 71; Indels 17; Gaps 5;  
1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKV 60  
1 MCGNHSKPPVFDENEVEVNFDFEILRAIGKSGFKVCIVQKRDTKMYAMKYNKQKV 60  
61 -ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFK 119  
61 QERDEVRNVFRELQIMQGLEHPLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFK 120  
120 EETVKLFICELVWALDYLNQRIIHRDMKPDNLLDEHGHVHTTDFNIAAMLPRETQITM 179

reproductive disorder.  
Homo sapiens.  
WO200138503-A2.  
31-MAY-2001.  
22-NOV-2000; 2000WO-US032085.  
24-NOV-1999; 99US-0167482P.  
(SUGE-) SUGEN INC.  
Florman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;  
Flanagan P, Clary D;  
WPI; 2001-343950/36.  
N-PSDB; AAS06704.  
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neural-associated diseases, and microbial infections.  
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encoding protein kinases and the polypeptides may be used in the  
prevention, diagnosis and treatment of diseases associated with  
inappropriate kinase expression. For example, they may be used to treat  
cancers (especially cancers of hematopoietic origin), cardiovascular  
disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),  
immune related diseases (e.g. rheumatoid arthritis), neurological  
disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.  
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disease (e.g. HIV) and reproductive disorders (e.g. infertility).  
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gene therapy and as DNA probes in diagnostic assays. The protein kinase  
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protein kinase expression and activity

Query Match 70.4%; Score 1513.5; DB 4; Length 327;  
Best Local Similarity 87.6%; Pred. No. 2.9e-135; Mismatches 19; Gaps 4;  
Matches 297; Conservative 5; Indels 19; Gaps 4;  
1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKV 60  
1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKV 60  
61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFK 120  
61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFK 120  
121 ETVKLFICELVWALDYLNQRIIHRDMKPDNLLDEHGHVHTTDFNIAAMLPRETQITM 180  
121 ETVKLFICELVWALDYLNQRIIHRDMKPDNLLDEHGHVHTTDFNIAAMLPRETQITM 180  
181 AGTKPMAEMSSRKAGYSAVDWWSLGVATYELLGRREPHYHRSSTSSKEIVHTFET 240  
181 AGTKPMAEMSSRKAGYSAVDWWSLGVATYELLGRREPHYHRSSTSSKEIVHTFET 240  
241 TVVTYPSAWSQEMVSLKKLLE-----PNPDQFQSLSVQ-----NPPYNDINWDVAFQKR 293  
241 TVVTYPSAWSQEMVSLKKVRRKTACPNVETKGRSLGSLSEVSIQY-----WGHQLSSL 295  
294 LIPGFTPNKGRINCDDTTFEELSEMLSKPLHKKKRLAK 332  
296 -----QKGRINCDDTTFEELSEMLSKPLHKKKRLAK 327

reproductive disorder.  
Homo sapiens.  
WO200138503-A2.  
31-MAY-2001.  
22-NOV-2000; 2000WO-US032085.  
24-NOV-1999; 99US-0167482P.  
(SUGE-) SUGEN INC.  
Florman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;  
Flanagan P, Clary D;  
WPI; 2001-343950/36.  
N-PSDB; AAS06704.  
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encoding protein kinases and the polypeptides may be used in the  
prevention, diagnosis and treatment of diseases associated with  
inappropriate kinase expression. For example, they may be used to treat  
cancers (especially cancers of hematopoietic origin), cardiovascular  
disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),  
immune related diseases (e.g. rheumatoid arthritis), neurological  
disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.  
Parkinson's disease), inflammatory disorders (e.g. asthma), infectious  
disease (e.g. HIV) and reproductive disorders (e.g. infertility).  
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against the protein kinases and in assays to identify modulators of  
protein kinase expression and activity

Query Match 70.4%; Score 1513.5; DB 4; Length 327;  
Best Local Similarity 87.6%; Pred. No. 2.9e-135; Mismatches 19; Gaps 4;  
Matches 297; Conservative 5; Indels 19; Gaps 4;  
1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKV 60  
1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKV 60  
61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFK 120  
61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFK 120  
121 ETVKLFICELVWALDYLNQRIIHRDMKPDNLLDEHGHVHTTDFNIAAMLPRETQITM 180  
121 ETVKLFICELVWALDYLNQRIIHRDMKPDNLLDEHGHVHTTDFNIAAMLPRETQITM 180  
181 AGTKPMAEMSSRKAGYSAVDWWSLGVATYELLGRREPHYHRSSTSSKEIVHTFET 240  
181 AGTKPMAEMSSRKAGYSAVDWWSLGVATYELLGRREPHYHRSSTSSKEIVHTFET 240  
241 TVVTYPSAWSQEMVSLKKLLE-----PNPDQFQSLSVQ-----NPPYNDINWDVAFQKR 293  
241 TVVTYPSAWSQEMVSLKKVRRKTACPNVETKGRSLGSLSEVSIQY-----WGHQLSSL 295  
294 LIPGFTPNKGRINCDDTTFEELSEMLSKPLHKKKRLAK 332  
296 -----QKGRINCDDTTFEELSEMLSKPLHKKKRLAK 327

reproductive disorder.  
Homo sapiens.  
WO200138503-A2.  
31-MAY-2001.  
22-NOV-2000; 2000WO-US032085.  
24-NOV-1999; 99US-0167482P.  
(SUGE-) SUGEN INC.  
Florman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;  
Flanagan P, Clary D;  
WPI; 2001-343950/36.  
N-PSDB; AAS06704.  
Nucleic acids encoding human kinase polypeptides, useful for preventing  
diagnosing and/or treating e.g. cancer, immune, cardiovascular and  
neural-associated diseases, and microbial infections.  
Claim 7; Fig 2; 433pp; English.  
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protein kinases have been identified as members of the tyrosine or  
serine/threonine kinase (PTK and STK) families. The polynucleotides  
encoding protein kinases and the polypeptides may be used in the  
prevention, diagnosis and treatment of diseases associated with  
inappropriate kinase expression. For example, they may be used to treat  
cancers (especially cancers of hematopoietic origin), cardiovascular  
disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),  
immune related diseases (e.g. rheumatoid arthritis), neurological  
disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.  
Parkinson's disease), inflammatory disorders (e.g. asthma), infectious  
disease (e.g. HIV) and reproductive disorders (e.g. infertility).  
Additionally, polynucleotides encoding protein kinases may be used for  
gene therapy and as DNA probes in diagnostic assays. The protein kinase  
polypeptides may be used as antigens in the production of antibodies  
against the protein kinases and in assays to identify modulators of  
protein kinase expression and activity

Query Match 70.4%; Score 1513.5; DB 4; Length 327;

121 EGTGKLYICELALALEYQRYHIIHRDIKPDNILLDEHGHVHTDNIATVILKGEKASS 180  
180 MAGTKYMAPEMPS--SRKGAGYSFAVDWWSLGVATAYELLRGRPPHYHRSSTSSKEIVHT 237  
181 MAGTKYMAPEMPS--SRKGAGYSFAVDWWSLGVATAYELLRGRPPHYHRSSTSSKEIVHT 240  
238 FETVTVTPSAWQEMVSLKLLKLEPNPQRFQSDVQNFPMNDINWDVAFQKRLIFG 297  
241 FKVERHYSTWCEGMVSLKLLKLEPNPQRFQSDVQNFPMNDINWDVAFQKRLIFG 300  
298 FPNKGRINCDPTFELEEMILESPLHKKKRLAK-KEKDMRKCDSSQTCLLQEHLDVQ 356  
301 FPNKGRINCDPTFELEEMILESPLHKKKRLAKHRSKSDTKDSCPLNGHLQCCLETVR 360  
357 KEFIIENREKVRNDFNKRQPNIALEQTKDPQVT--NGQMDTGLSETFTQSK 405  
361 KEFIIENREKLR-----QQHGDQLSLDGRIGSQTSKLDQGR 400

RESULT 10  
ABU62278  
ABU62278 standard; protein; 403 AA.

01-SEP-2003 (first entry)  
Human serine/threonine protein kinase #1.  
Human; enzyme; kinase; gene therapy; cancer; inflammation; psoriasis;  
arteriosclerosis.  
Homo sapiens.

US2003027307-A1.  
06-FEB-2003.  
26-SEP-2002; 2002US-00254869.  
09-MAR-2001; 2001US-00801876.  
(APPL-) APPLERA CORP.  
Ye J, Yan C, Di Francesco V, Beasley EM;  
WPI; 2003-492035/58.  
New isolated human kinase proteins, useful for treating disorders  
mediated by kinase pathway (e.g. cancers, inflammations, arteriosclerosis  
or psoriasis), or for development of human therapeutics and diagnostic  
compositions.

Disclosure; Fig 2B; 185pp; English.  
The invention relates to a new isolated human kinase peptide. The human  
kinase peptide and nucleic acid molecules are useful in the development  
of human therapeutics and diagnostic compositions. The peptides are  
useful for treating disorders (e.g. cancers, inflammations,  
arteriosclerosis or psoriasis) characterised by an absence of,  
inappropriate, or unwanted expression of the kinase protein. These  
molecules are particularly useful as models for developing human  
therapeutic targets, identifying therapeutic proteins, or serving as  
targets for the development of human therapeutic agents that modulate  
kinase activity in cells and tissues that express the kinase. The  
peptides are also useful for raising antibodies or eliciting an immune  
response; as a reagent (including the labelled reagent) in assays  
designed to quantitatively determine levels of the protein (or its  
binding partner or ligand) in biological fluids; or as markers for  
tissues in which the corresponding protein is preferentially expressed.  
The agents identified are useful for treating a subject with a disorder  
mediated by kinase pathway. The present sequence represents the amino  
acid sequence of the human serine/threonine protein kinase #1.

XX SQ Sequence= 403 AA;  
Query Match 66.2%; Score 1423.5; DB 6; Length 403;  
Best Local Similarity 72.3%; Pred. No. 1.5e-126;  
Matches 259; Conservative 40; Mismatches 60; Indels 3; Gaps 2;  
QY 1 MGANTSRKPPVDENEVDNFDHFEILRAIGKSPKVCIVQKNDTKMTAMKMKQKCV 60  
Db 1 MGNESHKPPVDENEVDNFDHFEILRAIGKSPKVCIVQKNDTKMTAMKMKQKCI 60  
QY 61 ERNEVRNFKELQIMQGLEHPELVNLWYSFQDEDMVVDLLGLDLYHQQNVHPKE 120  
Db 61 ERDEVRNFRERQIMQGLEHPELVNLWYSFQDEDMVVDLLGLDLYHQQNVHFT 120  
QY 121 ETVKLFICELVMDYLQNRHIIHRDMKPDNILLDEHGHVHTDNIAMLPRETQITTM 180  
Db 121 GIVKLYICELALALEYQRYHIIHRDIKPDNILLDEHGHVHTDNIATVILKGEKASS 180  
QY 181 AGTKYMAPEMPS--SRKGAGYSFAVDWWSLGVATAYELLRGRPPHYHRSSTSSKEIVHT 238  
Db 181 AGTKYMAPEMPS--SRKGAGYSFAVDWWSLGVATAYELLRGRPPHYHRSSTSSKEIVHT 240  
QY 239 ETTVTVTPSAWQEMVSLKLLKLEPNPQRFQSDVQNFPMNDINWDVAFQKRLIFG 298  
Db 241 KVERHYSTWCKGMVSLKLLKLEPNPQRFQSDVQNFPMNDINWDVAFQKRLIFG 300  
QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKRLAK-KEKDMRKCDSSQTCLLQEHLDVQ 357  
Db 301 FPNKGRINCDPTFELEEMILESPLHKKKRLAKHRSKSDTKDSCPLNGHLQCCLETVR 360  
QY 358 EFTIENREKVR 369  
Db 361 EFTIENREKLR 372

RESULT 11  
AAB65600  
ID AAB65600 standard; protein; 414 AA.  
XX AAB65600;  
XX AAB65600;  
DT 27-MAR-2001 (first entry)  
XX Novel protein kinase, SEQ ID NO: 125.  
DE Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;  
XX immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;  
KW dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;  
KW immune disorder; cardiovascular disease; neurodegenerative disease;  
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;  
KW inflammatory pelvic disease; multiple sclerosis; psoriasis.  
XX Homo sapiens.  
XX WO2000073469-A2.  
XX 07-DEC-2000.  
XX 26-MAY-2000; 2000WO-US014842.  
XX 28-MAY-1999; 99US-0136503P.  
XX (SUGS-) SUGEN INC.  
XX Plowmar. GD, Martinez R, Whyte D, Sudersanam S;  
XX WPI; 2001-032161/04.  
XX N-PSDB; AAF44625.  
XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and  
PT treating immune-related diseases and disorders, cardiovascular disease,  
PT neurodegenerative diseases and/or cancers.

XX PS Claim 10; Fig 1; 310pp; English.

XX CC The present sequence is a novel protein kinase. The novel protein kinases

XX CC and the nucleic acids that encode them may be used in the treatment and

XX CC diagnosis of diseases associated with inappropriate kinase expression

XX CC such as immune-related diseases and disorders, cardiovascular disease,

XX CC neurodegenerative diseases and/or cancers. The nucleic acids and

XX CC complementary sequences may also be used as DNA probes in diagnostic

XX CC assays. The kinase polypeptides may be used as antigens in the production

XX CC of antibodies of kinase expression and activity. Anti-kinase antibodies

XX CC and kinase antagonists may also be used to down regulate kinase

XX CC expression and activity. Diseases related to kinase expression and

XX CC activity include rheumatoid arthritis, atherosclerosis, autoimmune

XX CC disorders, complications of organ transplantation, myocardial infarction,

XX CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-

XX CC stress related disorders, chronic inflammatory bowel disease, chronic

XX CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,

XX CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive

XX CC disorders

XX PS Sequence 414 AA;

XX CC Query Match 66.2%; Score 1423.5; DB 4; Length 414;

XX CC Best Local Similarity 72.3%; Pred. No. 1.5e-126;

XX CC Matches 269; Conservative 40; Mismatches 60; Indels 3; Gaps 2;

QY 1 MGNANTSRKPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKCV 60

DB 1 MGNHSHKPPVFDENEVEVDFHFIQLRAIGKSGFKVCIVQKNDTKMYAMKYNKQKCI 60

QY 61 ERNEVRNVFKEIQMOGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVHFK 120

DB 61 ERDEVNRVRELQIQMOGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVHFE 120

QY 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHTDNIAMLPRETQITM 180

DB 121 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHTDNIATVVKGAERASS 180

QY 181 AGTKPYMAPEPFS--SRKAGYSFAVDWWSLGVATYELLGRPRPHIRSSSTSSKEIVHTF 238

DB 181 AGTKPYMAPEVQVYMDRPGYSYPVDWWSLGITAYELLGRWRPYEIHSTVTPIDELNMF 240

QY 239 ETTVTYPSAMSOEVMVSLIKLLEPNPQRSQSDVQNFYPMNDINMDAVFQKRLIPGF 298

DB 241 KVERVHYSTWCKGMVALLRKLITKDPESRVSSLDHIQSVPYLADNMWDVAFKKALMPGF 300

QY 299 IPNKGRLNCDPTFEELMLESKPLHKKKRLAK-KEKDMRKCDSSQTCLLQEHLDVQK 357

DB 301 VENKGRNLNCDPTFEELMLESKPLHKKKRLAKNRSDGTGKDCPLNGHLQHCLETVRE 360

QY 358 EPIIFNREKVN 369

DB 361 EPIIFNREKLRR 372

RESULT 12

ABP43807

ID ABP43807 standard; protein; 414 AA.

XX AC ABP43807;

XX DT 26-FEB-2003 (first entry)

XX DE Serine/threonine kinase.

XX KW Neuroprotective; immunomodulator; cancer; chromosome 4p16.1-p14;

XX KW cytotatic; anti-inflammatory; gene therapy; nutritional supplement;

XX KW wound; ulcer; Alzheimer's disease; Huntington's disease;

XX KW amyotrophic lateral sclerosis; autoimmune disorder; inflammation;

XX KW vulnery.

XX OS Homo sapiens.

XX PS Claim 20; SEQ ID # 710; 357pp + Sequence Listing; English.

XX CC The invention relates to 446 newly isolated polynucleotide sequences. The

XX CC activity of polynucleotides of the invention may be described as,

XX CC vulnery, neuroprotective, immunomodulator, cytostatic and anti-

XX CC inflammatory. Compositions comprising nucleic acids of the invention are

XX CC useful for treating a mammalian subject, or as nutritional sources or

XX CC supplements. These are useful in gene therapy, particularly for treating

XX CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,

XX CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or

XX CC inflammation. The nucleic acids and polypeptides are also useful in

XX CC diagnostic and research methods. The sequences given in records ABP4344-

XX CC ABP43989 represent polypeptides encoded by polynucleotides of the

XX CC invention. NOTE: The sequence data for this patent did not form part of

XX CC the printed specification, but was obtained in electronic format directly

XX CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX PS Sequence 414 AA;

XX CC Query Match 66.2%; Score 1423.5; DB 5; Length 414;

XX CC Best Local Similarity 72.3%; Pred. No. 1.5e-126;

XX CC Matches 269; Conservative 40; Mismatches 60; Indels 3; Gaps 2;

QY 1 MGNANTSRKPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKCV 60

DB 1 MGNHSHKPPVFDENEVEVDFHFIQLRAIGKSGFKVCIVQKNDTKMYAMKYNKQKCI 60

QY 61 ERNEVRNVFKEIQMOGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVHFK 120

DB 61 ERDEVNRVRELQIQMOGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVHFE 120

QY 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHTDNIAMLPRETQITM 180

DB 121 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHTDNIATVVKGAERASS 180

QY 181 AGTKPYMAPEPFS--SRKAGYSFAVDWWSLGVATYELLGRPRPHIRSSSTSSKEIVHTF 238

DB 181 AGTKPYMAPEVQVYMDRPGYSYPVDWWSLGITAYELLGRWRPYEIHSTVTPIDELNMF 240

QY 239 ETTVTYPSAMSOEVMVSLIKLLEPNPQRSQSDVQNFYPMNDINMDAVFQKRLIPGF 298

DB 241 KVERVHYSTWCKGMVALLRKLITKDPESRVSSLDHIQSVPYLADNMWDVAFKKALMPGF 300

QY 299 IPNKGRLNCDPTFEELMLESKPLHKKKRLAK-KEKDMRKCDSSQTCLLQEHLDVQK 357

DB 301 VENKGRNLNCDPTFEELMLESKPLHKKKRLAKNRSDGTGKDCPLNGHLQHCLETVRE 360

QY 358 EPIIFNREKVN 369

DB 361 EPIIFNREKLRR 372

RESULT 13  
AAO17710  
ID AAO17710 standard; protein; 414 AA.  
XX  
XX  
AC AAO17710;  
XX  
XX  
DT 20-AUG-2002 (first entry)  
XX  
XX  
DE Human serine-threonine protein kinase #2.  
XX  
XX  
KW Human; serine-threonine protein kinase; cancer; diabetes; obesity;  
KW central nervous system disorder; inflammation; gene therapy; COPD;  
KW neuroprotective; antiparkinsonian; cerebroprotective; cytostatic;  
KW antidiabetic; antiasthmatic; antihypertensive; anorectic;  
KW antiinflammatory; immunomodulator; chronic obstructive pulmonary disease;  
KW enzyme.  
XX  
XX  
OW Homo sapiens.  
XX  
XX  
PN WO200233056-A2.  
XX  
XX  
PD 25-APR-2002.  
XX  
XX  
PD 15-OCT-2001; 2001WO-EP011892.  
XX  
XX  
PD 16-OCT-2000; 2000US-0240097P.  
XX  
XX  
PD 30-JUL-2001; 2001US-0308096P.  
XX  
XX  
PD (FARB ) BAYER AG.  
XX  
XX  
PD Koehler RH;  
XX  
XX  
PD WPI; 2002-435534/46.  
XX  
XX  
PD New human serine-threonine protein kinase and encoding polynucleotides,  
PD useful for diagnosing, treating and preventing central nervous system  
PD disorders (e.g. stroke), diabetes, or cancers (e.g. leukemia).  
XX  
XX  
PD Disclosure; Fig 8; 135pp; English.  
XX  
XX  
PD The present invention provides the protein and coding sequences of a  
PD human serine-threonine protein kinase. The sequences can be used in the  
PD diagnosis, treatment and prevention of cancers (e.g. leukaemia, lymphoma  
PD or melanoma), CNS disorders (e.g. Parkinson's disease, stroke, or  
PD traumatic brain injury), diabetes, eating disorders (e.g. obesity,  
PD anorexia, or cachexia), allergies, anaphylaxis, asthma, inflammation and  
PD chronic obstructive pulmonary disease (COPD). The present sequence is a  
PD human serine-threonine protein kinase  
XX  
XX  
PD Sequence 414 AA;  
XX  
XX  
PD Query Match 66.2%; Score 1423.5; DB 5; Length 414;  
PD Best Local Similarity 72.3%; Pred. No. 1.5e-126;  
PD Matches 269; Conservative 40; Mismatches 60; Indels 3; Gaps 2;  
XX  
XX  
PD 1 MCANTSRKPPVFDENEDVNPDPHILRAIGKSGFKVCIVQNDTKQVAMKYNKQKV 60  
XX  
XX  
PD 1 MGNHSHKPPVFDENEDVNPDPHILRAIGKSGFKVCIVQNDTKQVAMKYNKQKV 60  
XX  
XX  
PD 61 ERNEVRNVFKELOIQMOGLEHPLNVLNWSFQDEDMFVVDLLGGDLRVHLOQNVHFE 120  
XX  
XX  
PD 61 ERDEVRNVFRELQIQMOGLEHPLNVLNWSFQDEDMFVVDLLGGDLRVHLOQNVHFE 120  
XX  
XX  
PD 121 ETVKLFICELVMDLYNQRIHRDMKPDNLLDEHGHVHTDFNTAAMLPRETQITTM 180  
XX  
XX  
PD 121 GTVKLYICELALAEYLQRYHIIHRDIKPDNLLDEHGHVHTDFNTATVYKGAERASSM 180  
XX  
XX  
PD 181 AGTKPYMAPEMFS--SRKAGYSPAVDWSLGVATAYELLGRPRPHINSSTSSKEIVHTF 238  
XX  
XX  
PD 181 AGTKPYMAPEVQVYMDRPGVSPYDWSLGVATAYELLGRPRPHINSSTSSKEIVHTF 238  
XX  
XX  
PD 239 ETTVVYTPSANSQEMVSLKLLLENFNPQPSQLSDVQNFPMYNDINWDVAFQKLLIPGF 298  
XX  
XX  
DB 241 KVERVHYSTWCKGMVALLRKLLTKDPESRVSLSLHDIGQVPIADNWDVAFKALMPGF 300  
QY 293 IFNKGRLNCDPTFELEEMILESPLHKKKKRLAK-KEKDMRKCDSSQTCCLQEHLDVOK 357  
DB 301 VFNKGRNCDPTFELEEMILESPLHKKKKRLAKNRSRDTGKDSQFLNGLHQCLETVRE 360  
QY 359 EFIIFNREKVR 369  
DB 361 EFIIFNREKLR 372  
XX  
XX  
DE Human cancer related protein SEQ ID NO:274.  
XX  
XX  
KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;  
KW heart disease; atherosclerosis; endometriosis.  
XX  
XX  
OW Homo sapiens.  
XX  
XX  
PN WO2003025138-A2.  
XX  
XX  
PD 27-MAR-2003.  
XX  
XX  
PD 17-SEP-2002; 2002WO-US029560.  
XX  
XX  
PD 17-SEP-2001; 2001US-0323469P.  
XX  
XX  
PD 20-SEP-2001; 2001US-0323887P.  
XX  
XX  
PD 13-NOV-2001; 2001US-0350666P.  
XX  
XX  
PD 08-FEB-2002; 2002US-0355145P.  
XX  
XX  
PD 08-FEB-2002; 2002US-0355257P.  
XX  
XX  
PD 12-APR-2002; 2002US-0372246P.  
XX  
XX  
PD (EOSB-) EOS BIOTECHNOLOGY INC.  
XX  
XX  
PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KB;  
PI Zlotnik A;  
XX  
XX  
DR WPI; 2003-354600/33.  
XX  
XX  
DR N-PSDB; ACC72764.  
XX  
XX  
PT New genes that are up-regulated or down-regulated in cancers, useful as  
PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as  
PT therapeutic targets for screening drugs for treating these diseases.  
XX  
XX  
PS Claim 12; Page 748; 767pp; English.  
XX  
XX  
CC The present invention describes an isolated nucleic acid molecule, which  
CC comprises the sequence of any of the genes that are up-regulated or down-  
CC regulated in specific cancers (e.g. about 1031 genes up-regulated in  
CC acute lymphocytic leukemia). ACC72841 to ACC72860 represent cancer  
CC related gene nucleotide sequences which encode the proteins given in  
CC ABR58521 to ABR58709. Also described: (1) determining the presence or  
CC absence of a pathological cell in a patient; (2) an expression vector  
CC comprising a nucleic acid molecule described above; (3) a host cell  
CC comprising the vector; (4) an isolated polypeptide, which is encoded by  
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide  
CC of (4); (6) specifically targeting a compound to a pathological cell in a  
CC patient by administering to the patient the antibody above; and (7) a  
CC drug screening assay. The nucleic acid is useful as diagnostic markers or  
CC therapeutic targets. In particular, the nucleic acid is useful for  
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,  
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,  
CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,  
CC atherosclerosis and endometriosis. The nucleic acid is also useful in  
CC drug screening, particularly for identifying agents for treating these





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: May 28, 2004, 02:30:27 ; Search time 523 Seconds  
(without alignments)  
9942.246 Million cell updates/sec

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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0  
Sequences: 3373863 seqs, 2124099041 residues  
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post processing: Minimum Match 0%  
Listing first 45 summaries

- Database : N Geneseq\_29Jan04.\*
- 1: geneseqn1980s.\*
  - 2: geneseqn1990s.\*
  - 3: geneseqn2000s.\*
  - 4: geneseqn2001as.\*
  - 5: geneseqn2001bs.\*
  - 6: geneseqn2002s.\*
  - 7: geneseqn2003as.\*
  - 8: geneseqn2003bs.\*
  - 9: geneseqn2003cs.\*
  - 10: geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1224	100.0	1224	6	AAD23678	Aad23678 Novel hum
2	1224	100.0	1675	6	AAD23680	Aad23680 Novel hum
3	1165.4	95.2	1191	6	AAD23679	Aad23679 Novel hum
4	1165.4	95.2	1594	4	AAd46891	Aad46891 CDNA enco
5	1165.4	95.2	1594	6	AAD34317	Aad34317 Human PKI
6	1163.8	95.1	1281	6	AAI70704	Aai70704 Human 149
7	1160.6	94.8	1485	7	AB554599	Ab554599 CDNA enco
8	1160.6	94.8	1485	8	ACA62840	Ac62840 CDNA enco
9	832.8	68.0	981	4	AAS06704	Aas06704 Polynucle
10	672.8	55.0	678	4	ABA08463	Aba08463 Human Ser
11	661	54.0	711	6	AAD23677	Aad23677 Novel hum
12	660	53.9	678	6	AAD23676	Aad23676 Novel hum
13	542.4	44.3	1587	6	ABQ61051	Abq61051 Serine/th
14	542.4	44.3	3224	4	AAFA4625	Aaf44625 Novel pro
15	542.4	44.3	3224	7	ADAI19317	Adai19317 Human ins
16	542.4	44.3	3224	9	ACC72764	Acc72764 Human can
17	542.4	44.3	3224	9	ADE38374	Ade38374 Human pro
18	519.6	42.5	3244	4	AAS46210	Aas46210 Human DNA
19	519.6	42.5	3244	7	ABX78813	Abx78813 Human PRO
20	519.6	42.5	3244	7	ACA75785	Aca75785 Novel hum
21	519.6	42.5	3244	7	ACA71265	Aca71265 Human sec
22	519.6	42.5	3244	7	ACC87793	Acc87793 Human sec
23	519.6	42.5	3244	7	ACC87179	Acc87179 Human sec

24	519.6	42.5	3244	7	ACD04352	Acd04352 Human sec
25	519.6	42.5	3244	7	ACA69683	Aca69683 CDNA enco
26	519.6	42.5	3244	7	ACA90528	ACA90528 Novel hum
27	519.6	42.5	3244	7	ACC89635	Acc89635 Human sec
28	519.6	42.5	3244	7	ACA98426	ACA98426 Novel hum
29	519.6	42.5	3244	7	ACA94068	Aca94068 Human sec
30	519.6	42.5	3244	7	ACD15461	Acd15461 Human sec
31	519.6	42.5	3244	7	ACD09048	Acd09048 Human sec
32	519.6	42.5	3244	7	ACC96968	Acc96968 Human sec
33	519.6	42.5	3244	7	ACF15689	Acf15689 Human sec
34	519.6	42.5	3244	7	ACA73056	Aca73056 Human PRO
35	519.6	42.5	3244	7	ACD03228	Acd03228 Novel hum
36	519.6	42.5	3244	7	ACD02043	Acd02043 Novel hum
37	519.6	42.5	3244	7	ACA92235	ACA92235 Novel hum
38	519.6	42.5	3244	7	ACA89660	Aca89660 CDNA enco
39	519.6	42.5	3244	7	ACA73670	Aca73670 Human sec
40	519.6	42.5	3244	7	ACA05985	Aca05985 Human sec
41	519.6	42.5	3244	7	ACA66819	Aca66819 CDNA enco
42	519.6	42.5	3244	7	ACF20394	Acf20394 Human sec
43	519.6	42.5	3244	7	ACF19780	Acf19780 Human sec
44	519.6	42.5	3244	7	ACD22068	Acd22068 Human sec
45	519.6	42.5	3244	7	ACF13233	Acf13233 Human sec

ALIGNMENTS

RESULT 1  
AAD23678  
ID AAD23678 standard; CDNA; 1224 BP.

XX  
AC AAD23678;

XX  
DT 07-MAR-2002 (first entry)

XX  
DE Novel human protein (NHP) kinase CDNA #3.

XX  
KW Novel human protein; NHP; gene therapy; diagnosis; drug screening;  
KW gene expression; breast cancer; prostate cancer; nutritional; cosmetic;  
KW medical disorder; mental; biological; physiological; chemotherapeutic;  
KW ss.

XX  
OS Homo sapiens.

XX  
FH Key

XX  
CDS Location/Qualifiers

FT 1..1224

FT /\*tag= a

FT /product= "Novel human protein (NHP) kinase"

XX  
WO200181557-A2.

XX  
01-NOV-2001.

XX  
24-APR-2001; 2001WO-US013149.

XX  
25-APR-2000; 2000US-0199499P.

XX  
01-MAY-2000; 2000US-0201227P.

XX  
(LEXI-) LEXICON GENETICS INC.

XX  
Hu Y, Nepomnichy B, Wang X, Donoho G, Scoville J, Walke DW;

XX  
WPI; 2002-034442/04.

XX  
P-PSDB; AAE14260.

XX  
PT New nucleic acid molecules encoding new human proteins, useful in  
PT diagnosis, drug screening, clinical trial monitoring, treatment of  
PT physiological disorders, and cosmetic or nutritional applications.  
XX  
PS Claim 4; Page 41; 44pp; English.  
XX  
CC The invention relates to novel human protein (NHP) kinases and their  
CC corresponding CDNA molecules. NHP kinase and its DNA are useful as

reagents in assays for screening compounds that can be used as  
pharmaceutical reagents useful in the therapeutic treatment of mental,  
biological and medical disorders, and also as chemotherapeutic agents  
useful in the treatment of breast cancer and prostate cancer. NHP DNA is  
useful for diagnosis, drug screening, clinical trial monitoring, the  
treatment of physiological disorders or diseases, and cosmetic and  
nutritional applications. NHP DNA is also useful for the identification  
of coding sequence and the mapping of a unique gene to a particular  
chromosome. NHP DNA is further useful as hybridisation probes for  
screening libraries and assessing gene expression patterns, and also for  
the detection of mutant NHPs or inappropriately expressed NHPs for  
disease diagnosis. NHP DNA is also useful in gene therapy. The present  
sequence is novel human protein (NHP) kinase cDNA which is similar to  
serine/threonine protein kinases, ribosomal protein kinases and cAMP-  
dependent kinases cDNA related to the invention

Sequence 1224 BP; 381 A; 263 C; 283 G; 297 T; 0 U; 0 Other;  
Very Match 100.0%; Score 1224; DB 6; Length 1224;  
Fast Local Similarity 100.0%; Pred. No. 0;  
Matches 1224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGAGCCCACTTCAAGAAACCAACCAAGTGTGATCAAAATGAAGATGTCAACTT 60  
1 ATGGAGCCCACTTCAAGAAACCAACCAAGTGTGATCAAAATGAAGATGTCAACTT 60  
61 GACCACCTTGAATTTTGGAGCCATTGGGAAAGCGAGTTTGGGAGGTCTCATGTGA 120  
61 GACCACCTTGAATTTTGGAGCCATTGGGAAAGCGAGTTTGGGAGGTCTCATGTGA 120  
121 CAGAAGATGATACCAAGAGATGTAGCGAATGAAGTACATGATTAACAACAAAGTGGTG 180  
121 CAGAAGATGATACCAAGAGATGTAGCGAATGAAGTACATGATTAACAACAAAGTGGTG 180  
181 GAGCGCAATGAGTGAAGATGTCTTCAAGAACTCCAGATCATGAGGCTCTGGAGCAC 240  
181 GAGCGCAATGAGTGAAGATGTCTTCAAGAACTCCAGATCATGAGGCTCTGGAGCAC 240  
241 CCTTCTCTGTTAATTTGTGTTATTCCTTCAAGATGAGGAGACATGTTTCATGGTGGT 300  
241 CCTTCTCTGTTAATTTGTGTTATTCCTTCAAGATGAGGAGACATGTTTCATGGTGGT 300  
301 GACTCTCTGTTGAGACCTGCGTTATCCTGCAAGACAGACGTCCTCAAGGAA 360  
301 GACTCTCTGTTGAGACCTGCGTTATCCTGCAAGACAGACGTCCTCAAGGAA 360  
361 GAAACAGTGAAGTCTTCACTGTGAGCTGTGATGCTGAGTCTGAGTCTGAGGAAACAG 420  
361 GAAACAGTGAAGTCTTCACTGTGAGCTGTGATGCTGAGTCTGAGTCTGAGGAAACAG 420  
421 CGCATCATTCACAGGGATATGAAGCTTGACAAATATTTTACTGACGAACATGGGACGTG 480  
421 CGCATCATTCACAGGGATATGAAGCTTGACAAATATTTTACTGACGAACATGGGACGTG 480  
481 CACATCAGATTTCAACATGCTGCGATGCTGCCAGGGAGACACAGATTTACCCCATG 540  
481 CACATCAGATTTCAACATGCTGCGATGCTGCCAGGGAGACACAGATTTACCCCATG 540  
541 GCTGGCACCAAGCTTACATGGCACTTGAGATGTTCAAGTCTCAGAAAGGAGCAGGCTAT 600  
541 GCTGGCACCAAGCTTACATGGCACTTGAGATGTTCAAGTCTCAGAAAGGAGCAGGCTAT 600  
601 TCCTTTGCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
601 TCCTTTGCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
661 AGACCGTATCATATTCGCTCAGTACTTCCAGCAAGGAATTTGACACAGTTTGGAGCG 720  
661 AGACCGTATCATATTCGCTCAGTACTTCCAGCAAGGAATTTGACACAGTTTGGAGCG 720  
721 ACTGTGTGAACCTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
721 ACTGTGTGAACCTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780

781 CTCGAACCTTAATCCAGACCAACAGATTTTCTAGTTATCTGATGTCCAGAACTTCCGGTAT 840  
781 CTCGAACCTTAATCCAGACCAACAGATTTTCTAGTTATCTGATGTCCAGAACTTCCGGTAT 840  
841 ATGAATGATATAAATCTGGATCAGTTTTCAGAGAGGCTCATTCAGGTTTCATTCCT 900  
841 ATGAATGATATAAATCTGGATCAGTTTTCAGAGAGGCTCATTCAGGTTTCATTCCT 900  
901 AATAAGGAGGAGCTGAATTTGATCTTCTTGAACCTTGAAGAAATGATTTTGAGTCC 960  
901 AATAAGGAGGAGCTGAATTTGATCTTCTTGAACCTTGAAGAAATGATTTTGAGTCC 960  
961 AAACCTCTACATAAGAAAAAGGCTCTGGCAAGAGAGAGATATGAGGAATGC 1020  
961 AAACCTCTACATAAGAAAAAGGCTCTGGCAAGAGAGAGATATGAGGAATGC 1020  
1021 GATTTCTTCTCAGACATGTTCTTCTCAAGAGACCTTGAATCTGTCCAGAGGATTCATA 1080  
1021 GATTTCTTCTCAGACATGTTCTTCTCAAGAGACCTTGAATCTGTCCAGAGGATTCATA 1080  
1081 ATTTTCAACAGAGAAAAAGTAAACAGGGACTTTTAAACAAAGACACCAATCTAGCCTTG 1140  
1081 ATTTTCAACAGAGAAAAAGTAAACAGGGACTTTTAAACAAAGACACCAATCTAGCCTTG 1140  
1141 GAACAAACCAAGACCCACAGTGAATGGAACAAATGGAACAAATGGAACAAATGGAACAA 1200  
1141 GAACAAACCAAGACCCACAGTGAATGGAACAAATGGAACAAATGGAACAAATGGAACAA 1200  
1201 TTTTCAGACCTCGAAAGTTTTCATAA 1224  
1201 TTTTCAGACCTCGAAAGTTTTCATAA 1224

RESULT 2  
AAD23680  
ID AAD23680 standard; DNA; 1675 BP.  
XX AAD23680;  
DT 07-MAR-2002 (first entry)  
XX Novel human protein (NHP) kinase full-length ORF and flanking region DNA.  
XX Novel human protein; NHP; gene therapy; diagnosis; drug screening;  
KW gene expression; breast cancer; prostate cancer; nutritional; cosmetic;  
KW medical disorder; mental; biological; physiological; chemotherapeutic;  
ds.  
XX Homo sapiens.  
XX WO200181557-A2.  
PN 01-NOV-2001.  
PD 24-APR-2001; 2001WO-US013149.  
PF 25-APR-2000; 2000US-0199499P.  
PR 01-MAY-2000; 2000US-0201227P.  
XX (LEXI-) LEXICON GENETICS INC.  
XX Hu Y, Nepomnichy B, Wang X, Donoho G, Scoville J, Walke DW;  
PI WPI; 2(02-034442/04.  
XX New nucleic acid molecules encoding new human proteins, useful in  
PT diagnosis, drug screening, clinical trial monitoring, treatment of  
PT physiological disorders, and cosmetic or nutritional applications.  
XX Disclosure; Page 44; 44pp; English.  
XX The invention relates to novel human protein (NHP) kinases and their

corresponding cDNA molecules. NHP kinase and its DNA are useful as reagents in assays for screening compounds that can be used as pharmaceutical reagents useful in the therapeutic treatment of mental, biological and medical disorders, and also as chemotherapeutic agents useful in the treatment of breast cancer and prostate cancer. NHP DNA is useful for diagnosis, drug screening, clinical trial monitoring, the treatment of physiological disorders or diseases, and cosmetic and nutritional applications. NHP DNA is also useful for the identification of coding sequence and the mapping of a unique gene to a particular chromosome. NHP DNA is further useful as hybridisation probes for screening libraries and assessing gene expression patterns, and also for the detection of mutant NHPs or inappropriately expressed NHPs for disease diagnosis. NHP DNA is also useful in gene therapy. The present sequence is novel human protein (NHP) kinase full-length ORF (open reading frame) and flanking region DNA related to the invention

Sequence 1675 BP; 469 A; 404 C; 414 G; 388 T; 0 U; 0 Other;

Very Match 100.0%; Score 1224; DB 6; Length 1675;

Local Similarity 100.0%; Pred. No. 0;

Mismatches 1224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGAGGCAACATCTCAAGAAACCCACGCTGTTGATGAAATGAAGATGTCACCTTT 60

413 ATGGAGGCAACATCTCAAGAAACCCACGCTGTTGATGAAATGAAGATGTCACCTTT 472

61 GACCACTTTGAAATTTTGGAGCCATGGGAAGGCGAGTTTGGGAAGGCTGCAATTGTA 120

473 GACCACTTTGAAATTTTGGAGCCATGGGAAGGCGAGTTTGGGAAGGCTGCAATTGTA 532

121 CAGAAAGATGATACCAAGAAGATGACGAATGAAGTACATGAATTAACAAGTGGCGTG 180

533 CAGAAAGATGATACCAAGAAGATGACGAATGAAGTACATGAATTAACAAGTGGCGTG 592

181 GAGCCCAATGAAGTACGAATGCTTCAAGAACTCCAGATCATCAGGCTCTGAGCAC 240

593 GAGCCCAATGAAGTACGAATGCTTCAAGAACTCCAGATCATCAGGCTCTGAGCAC 652

241 CTTTCTCTGGTTAAATTTGTGGTATTCCTTCAAGATGAGAAAGATGTTCAATGTTGGTG 300

653 CTTTCTCTGGTTAAATTTGTGGTATTCCTTCAAGATGAGAAAGATGTTCAATGTTGGTG 712

301 GACCTCTCTGGTGGAGACCTGGGTTATACCTGCAACAGAACTGCATTTCAAGGAA 360

713 GACCTCTCTGGTGGAGACCTGGGTTATACCTGCAACAGAACTGCATTTCAAGGAA 772

361 GAAACAGTGAAGCTCTTCACTGTGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 420

773 GAAACAGTGAAGCTCTTCACTGTGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 832

421 CGCATCATTCAGGGATATGAAGCTGACATATATTTTACGCAACATGGGCACTG 480

833 CGCATCATTCAGGGATATGAAGCTGACATATATTTTACGCAACATGGGCACTG 892

481 CACATCACAGATTTCAACATGCTGGATGCTGGCCAGGAGACACAGATTAACCCATG 540

893 CACATCACAGATTTCAACATGCTGGATGCTGGCCAGGAGACACAGATTAACCCATG 952

541 GCTGGACCAAGCTTACATGAGCACTGAGATGTTCCAGTCCAGAAAGAGAGGCTAT 600

953 GCTGGACCAAGCTTACATGAGCACTGAGATGTTCCAGTCCAGAAAGAGAGGCTAT 1012

601 TCCTTTGCTGTTGACCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 660

1013 TCCTTTGCTGTTGACCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1072

661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATGTAACAGTTTGAGAG 720

1073 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATGTAACAGTTTGAGAG 1132

721 ACTGTTGTAATTAACCTTCTGCTGGTGCACAGGAAATGCTGTCATCTTTAAAGCTTA 780

1133 ACTGTTGTAATTAACCTTCTGCTGGTGCACAGGAAATGCTGTCATCTTTAAAGCTTA 1192

781 CTGGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT 840

1193 CTGGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT 1252

841 ATGAATGATATAAATCGGATGCGATGTTTTCAGAAAGGCGCTCATTCAGGTTTCATTCCT 900

1253 ATGAATGATATAAATCGGATGCGATGTTTTCAGAAAGGCGCTCATTCAGGTTTCATTCCT 1312

901 AATAAAGCGAGGCTGAATGTGATGCTTACCTTTGAACTTGAGGAAATGATTTTGGAGTCC 960

1313 AATAAAGCGAGGCTGAATGTGATGCTTACCTTTGAACTTGAGGAAATGATTTTGGAGTCC 1372

961 AAACCTCTACATAGAAAAGGCTGCGCAAGGAGGAGGAGGATATGAGGAAATGC 1020

1373 AAACCTCTACATAGAAAAGGCTGCGCAAGGAGGAGGAGGATATGAGGAAATGC 1432

1021 GATTCTTCTCAGACATGCTTCTTCAAGAGCACCTTGACTCTGTCAGAAAGGAGTTTCATA 1080

1433 GATTCTTCTCAGACATGCTTCTTCAAGAGCACCTTGACTCTGTCAGAAAGGAGTTTCATA 1492

1081 ATTTTCAACAGAGAAAAGTAAACAGGAGCTTTTAAACAAAAGACAAACCAAAATCTAGCCTTG 1140

1493 ATTTTCAACAGAGAAAAGTAAACAGGAGCTTTTAAACAAAAGACAAACCAAAATCTAGCCTTG 1552

1141 GAACAAACCAAGACCCCAAGTCAAAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 1200

1553 GAACAAACCAAGACCCCAAGTCAAAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 1612

1201 TTTTCAGACCTCGAAAGTTTCATAA 1224

1613 TTTTCAGACCTCGAAAGTTTCATAA 1636

RESULT 3

AAD23679 standard; cDNA; 1191 BP.

XX AAD23679;

AC AC

DT 07-MAR-2002 (first entry)

XX Novel human protein (NHP) kinase cDNA #4.

XX Novel human protein; NHP; gene therapy; diagnosis; drug screening;

KW gene expression; breast cancer; prostate cancer; nutraceutical; cosmetic;

KW medical disorder; mental; biological; physiological; chemotherapeutic;

XX ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FH 1..1191

FT /\*tag= a

ET /product= "Novel human protein (NHP) kinase"

XX WO200181557-A2.

XX 01-NOV-2001.

XX 24-APR-2001; 2001WO-US013149.

XX 25-APR-2000; 2000US-0199499P.

PR 01-MAY-2000; 2000US-0201227P.

XX (LEXI-) LEXICON GENETICS INC.

XX Hu Y, Nepomnichy B, Wang X, Donoho G, Scoville J, walke DW;

PI WPI; 2002-034442/04.

XX P-PSDB; AAE14261.

XX New nucleic acid molecules encoding new human proteins, useful in

PT

diagnosis, drug screening, clinical trial monitoring, treatment of physiological disorders, and cosmetic or nutraceutical applications.

Claim 7; Page 42; 44pp; English.

The invention relates to novel human protein (NHP) kinases and their corresponding cDNA molecules. NHP kinase and its DNA are useful as reagents in assays for screening compounds that can be used as pharmaceutical reagents useful in the therapeutic treatment of mental, biological and medical disorders, and also as chemotherapeutic agents useful in the treatment of breast cancer and prostate cancer. NHP DNA is useful for diagnosis, drug screening, clinical trial monitoring, the treatment of physiological disorders or diseases, and cosmetic and nutraceutical applications. NHP DNA is also useful for the identification of coding sequence and the mapping of a unique gene to a particular chromosome. NHP DNA is further useful as hybridisation probes for screening libraries and assessing gene expression patterns, and also for the detection of mutant NHPs or inappropriately expressed NHPs for disease diagnosis. NHP DNA is also useful in gene therapy. The present sequence is novel human protein (NHP) kinase cDNA which is similar to serine/threonine protein kinases, ribosomal protein kinases and CAMP-dependent kinases cDNA related to the invention

Sequence 1191 BP; 369 A; 254 C; 278 G; 290 T; 0 U; 0 Other;

Sequence Match 95.2%; Score 1165.4; DB 6; Length 1191; 1st Local Similarity 99.1%; Pred. No. 0; Matches 1172; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

1 ATGGGAGCCAACTTCAAGAAACACACAGTGTGTTGATGAAATCAAGATGTCAACTTT 60  
1 ATGGGAGCCAACTTCAAGAAACACACAGTGTGTTGATGAAATCAAGATGTCAACTTT 60  
61 GACCACTTTGAAATTTGGGAGCCATTGGGAAAGGAGTGTGGGAGGCTTGCATTGTA 120  
61 GACCACTTTGAAATTTGGGAGCCATTGGGAAAGGAGTGTGGGAGGCTTGCATTGTA 120  
121 CAGAAATGATCAAGAGATGTGACCAATCAAGTACATGATGATGATGATGATGATGATG 180  
121 CAGAAATGATCAAGAGATGTGACCAATCAAGTACATGATGATGATGATGATGATGATG 180  
181 GAGCGCAATGAGTGAAGTGTCTTCAAGAACTCCAGATCATGACAGGCTCTGGAGCAC 240  
181 GAGCGCAATGAGTGAAGTGTCTTCAAGAACTCCAGATCATGACAGGCTCTGGAGCAC 240  
241 CCTTCTCTGTTAAATTTGGTATTCCTTCAAGATGAGGAGACATGTTTATGTTGGTG 300  
241 CCTTCTCTGTTAAATTTGGTATTCCTTCAAGATGAGGAGACATGTTTATGTTGGTG 300  
301 GACCTCTCTGGTGGAGACCTGGTATTCACCTGCAAGACCTGCAAGACCTGCAAGAA 360  
301 GACCTCTCTGGTGGAGACCTGGTATTCACCTGCAAGACCTGCAAGACCTGCAAGAA 360  
361 GAAACAGTGAAGCTCTTCACTGTGAGCTGGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 420  
361 GAAACAGTGAAGCTCTTCACTGTGAGCTGGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 420  
421 CGCATCATTCACAGGATATGAGGCTGCAAAATTTTACTTCAAGAAATGAGGAGGAGT 480  
421 CGCATCATTCACAGGATATGAGGCTGCAAAATTTTACTTCAAGAAATGAGGAGGAGT 480  
481 CACATCAGATTTCAACATTTGCTGGATGCTGCCAGGAGACACAGATTTACCATG 540  
481 CACATCAGATTTCAACATTTGCTGGATGCTGCCAGGAGACACAGATTTACCATG 540  
541 GCTGGCACCAGCTTACATGGCACTTGGATGTTTCAAGTCCAGAAAGGAGGAGGCTAT 600  
541 GCTGGCACCAGCTTACATGGCACTTGGATGTTTCAAGTCCAGAAAGGAGGAGGCTAT 600  
601 TCCTTTCTGTTGATGCTGGTGGTCCCTGGAGTACGAGCATATGAACTGCTGAGAGCCGG 660  
601 TCCTTTCTGTTGATGCTGGTGGTCCCTGGAGTACGAGCATATGAACTGCTGAGAGCCGG 660

QY 66. AGACGATATATATTCGCTCCAGTACTTCCAGCAAGGAAATGTACACACGTTTGGAGCG 720  
DB 66. AGACGATATATATTCGCTCCAGTACTTCCAGCAAGGAAATGTACACACGTTTGGAGCG 720  
QY 72.1 ACTGTTGTAACCTTACCCCTTCTGCTGGTGCACAGGAAATGGTGTCACTTCTTAAAAAGCTA 780  
DB 72.1 ACTGTTGTAACCTTACCCCTTCTGCTGGTGCACAGGAAATGGTGTCACTTCTTAAAAAGCTA 780  
QY 78.1 CTCGAACTTATCCAGACCAAGGATTTCTCAGTTATCTGATGTCGAGAACTTCCCGTAT 840  
DB 78.1 CTCGAACTTATCCAGACCAAGGATTTCTCAGTTATCTGATGTCGAGAACTTCCCGTAT 840  
QY 84.1 ATGAATGATATAAATCTGGATGTCAGTCTTTCAGAAAGGCTCATTCAGGTTTCATTCCT 900  
DB 84.1 ATGAATGATATAAATCTGGATGTCAGTCTTTCAGAAAGGCTCATTCAGGTTTCATTCCT 900  
QY 90.1 AATAAGGAGCTGCAATTTGATCTCCTTGAACCTTGAAGAAATGATTTGGAGTCC 960  
DB 90.1 AATAAGGAGCTGCAATTTGATCTCCTTGAACCTTGAAGAAATGATTTGGAGTCC 960  
QY 96.1 AAACCTCTACATAAGAAAGGCTCTGCAAGAGGAGGAGGATATGAGGAAATGC 1020  
DB 96.1 AAACCTCTACATAAGAAAGGCTCTGCAAGAGGAGGAGGATATGAGGAAATGC 1020  
QY 102.1 GATTCCTCTCAGACATGCTCTTCAAGAGCACCTTGTCTGTCCAGAGGAGTTCATA 1080  
DB 102.1 GATTCCTCTCAGACATGCTCTTCAAGAGCACCTTGTCTGTCCAGAGGAGTTCATA 1080  
QY 108.1 ATTTTCAACAGAGAAAGTAAACAGGAGCTTTAAACAAAGGAGGAGGATATGAGGAAATGC 1140  
DB 108.1 ATTTTCAACAGAGAAAGTAAACAGGAGCTTTAAACAAAGGAGGAGGATATGAGGAAATGC 1140  
QY 114.1 GAACAAACCAAGAGCCCAAGTGCAGAAATGAGGAGGAGGATATGAGGAAATGC 1183  
DB 114.1 GAACAAACCAAGAGCCCAAGTGCAGAAATGAGGAGGAGGATATGAGGAAATGC 1183  
RESULT 4  
AAH46891  
ID AAH46891 standard; cDNA; 1594 BP.  
XX  
AC AAH46891;  
XX  
DT 25-SEP-2001 (first entry)  
XX  
DE cDNA encoding human protein kinase SGK177.  
XX  
KW Protein kinase; enzyme; cytostatic; nootropic; neuroprotective; human;  
KW antiparkinsonian; virucide; antibacterial; antifungal; antimigraine;  
KW analgesic; hypotensive; hypertensive; immunosuppressive; antiallergic;  
KW antipsoriatic; antirheumatic; antidiabetic; antihypertensive; anorectic;  
KW osteoprotic; thrombolytic; antiarteriosclerotic; antiasthmatic;  
KW vasotropic; antidiabetic; gene therapy; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 404..1594  
FT /\*tag= a  
XX  
PN WO200155356-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 25-JAN-2001; 2001WO-US002337.  
XX  
PR 25-JAN-2000; 2000US-0178078P.  
PR 31-JAN-2000; 2000US-0179364P.  
PR 17-FEB-2000; 2000US-0183173P.  
PR 17-MAR-2000; 2000US-0190162P.  
PR 29-MAR-2000; 2000US-0193404P.  
PR 13-NOV-2000; 2000US-0247013P.  
XX









Human; kinase; serine/threonine kinase; immune response; transgenic;  
Gene therapy; chromosome 5; gene; ss.  
Homo sapiens.

Key Location/Qualifiers  
5'UTR 1..2  
/\*tag= a  
3..1193  
/\*tag= b  
CDS /product= "Serine/threonine protein kinase-like kinase"  
1194..1485  
3'UTR /\*tag= c

US2002127683-A1.

12-SEP-2002.

09-MAR-2001; 2001US-00801876.

09-MAR-2001; 2001US-00801876.

(YEJ)/ YE J.

(YANC)/ YAN C.

(DFRA)/ DI FRANCESCO V.

(BEAS)/ BEASLEY E M.

Ye J, Yan C, Di Francesco V, Beasley EM;

WPI; 2003-028938/02.

P-PSDB; ABG70700.

Novel isolated human kinase peptide useful for treating disorder  
characterized by absence of, in appropriate or unwanted expression of the  
kinase protein, and as immunogens to raise antibodies.

Claim 4; Fig 1; 174pp; English.

The present invention relates to the isolation of a human kinase and the  
polynucleotide sequences encoding it. The human kinase of the invention  
is related to the serine/threonine kinase subfamily. The gene encoding  
the human kinase is located on chromosome 5. The polypeptide and  
polynucleotide sequences of the invention are useful for treating a  
disease or condition mediated by a human kinase. Both the polypeptide and  
polynucleotide sequences are useful as models for the development of  
human therapeutics, for identifying therapeutic proteins, as targets for  
development of human therapeutic agents, and as query sequences to  
perform a search against sequence data bases to identify other family  
members of related sequences. The polypeptide is useful to raise  
antibodies or to elicit another immune response, as a reagent in assays  
designed to quantitatively determine levels of the protein in biological  
fluids, as markers for tissues in which the corresponding protein is  
preferentially expressed, in drug screening assays, in cell-based or cell  
-free systems, to identify compounds that modulate kinase activity of the  
protein in its natural state, or an altered form that causes the specific  
disease or pathology associated with the kinase, to screen a compound for  
the ability to stimulate or inhibit interaction between the kinase  
protein and a molecule that normally interacts with the kinase protein,  
and in pharmacogenomic analysis. The polynucleotide is useful for  
monitoring the effectiveness of modulating compounds on the expression or  
activity of the human kinase gene in clinical trials or in a treatment  
regimen, in diagnostic assays for qualitative changes in a human kinase  
nucleic acid that leads to a pathology, for testing an individual for a  
genotype that while not necessarily causing a disease, nevertheless  
affects the treatment modality, as antisense constructs to control human  
kinase gene expression in cells, tissues and organisms, for gene therapy  
in patients containing cells that are aberrant in human kinase gene  
expression, and to produce transgenic animals. The present sequence  
encodes a human kinase related to the serine/threonine protein kinase  
subfamily

Sequence 1485 BP; 471 A; 316 C; 331 G; 367 T; 0 U; 0 Other;

Query Match	94.8%;	Score 1160.6;	DB 7;	Length 1485;
Best Local Similarity	98.8%;	Pred. No. 0;		
Matches 1159;	Conservative 0;	Mismatches 14;	Indels 0;	Gaps 0;
QY	1	ATGGGAGCCAAACACATTCAAGAAAAACCAACAGTGTTCATGAAAAATGAAGATGTCAACTTT	60	
DB	3	ATGGGAGCCAAACACATTCAAGAAAAACCAACAGTGTTCATGAAAAATGAAGATGTCAACTTT	62	
QY	61	GACCACTTTGAAATTTGGAGCCATTGGGAAAGGCAGTTTGGGAAGGTCATGCAATGTA	120	
DB	63	GACCACTTTGAAATTTGGAGCCATTGGGAAAGGCAGTTTGGGGAGGTCATGCAATGTA	122	
QY	121	CAGAAGAAATGATACCAAGAGAGTGTACGCAATCAAGTACATGAATAAACAAGATGCGTG	180	
DB	123	CAGAAGAAATGATACCAAGAGAGTGTGCGCAATGAGTACATGAATAAACAAGTGGTG	182	
QY	181	GAGCGCAATGAAAGTGAAGAAATGCTTCAAGGAACTCCAGATCATGACAGGCTCTGGAGCAC	240	
DB	183	GAGCGCAATGAAAGTGAAGAAATGCTTCAAGGAACTCCAGATCATGACAGGCTCTGGAGCAC	242	
QY	241	CTTTTCTGCTGTTAATTTGTGGTATTCCTTCCAAAGATGAGGAAGACATGTTTCATGTTGGTG	300	
DB	243	CTTTTCTGCTGTTAATTTGTGGTATTCCTTCCAAAGATGAGGAAGACATGTTTCATGTTGGTG	302	
QY	301	GACCTCTGCTGGTGAGACCTGCGTTATTCAGTCAACAGAACTCCACTTCAAGGAA	360	
DB	303	GACCTCTGCTGGTGAGACCTGCGTTATTCAGTCAACAGAACTCCACTTCAAGGAA	362	
QY	361	GAACAGTGAAGCTCTTCATCTGTGAGCTGGTTCATGCGCTGAGCTACCTGCAAGAACG	420	
DB	363	GAACAGTGAAGCTCTTCATCTGTGAGCTGGTTCATGCGCTGAGCTACCTGCAAGAACG	422	
QY	421	CGCATCATTCAGAGGATGAGAGCTGCAATATTTTACTTGACGAACATGGGACGCTG	480	
DB	423	CGCATCATTCAGAGGATGAGAGCTGCAATATTTTACTTGACGAACATGGGACGCTG	482	
QY	481	CACATCACAGATTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATTACACCATG	540	
DB	483	CACATCACAGATTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATTACACCATG	542	
QY	541	GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCAGCTTCCAGAAAGGAGGAGGCTAT	600	
DB	543	GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCAGCTTCCAGAAAGGAGGAGGCTAT	602	
QY	601	TCCTTTGCTGTTGACCTGGTGCTCCCTGGGAGTGACGGCATATGAACTGCTGAGAGGCGG	660	
DB	603	TCCTTTGCTGTTGACCTGGTGCTCCCTGGGAGTGACGGCATATGAACTGCTGAGAGGCGG	662	
QY	661	AGACCGTATCATATTTGCTCCAGTACTTCAGCAAGGAAATTTGACACAGTTTGAGACG	720	
DB	663	AGACCGTATCATATTTGCTCCAGTACTTCAGCAAGGAAATTTGACACAGTTTGAGACG	722	
QY	721	ACTGTTGTAATTTTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	780	
DB	723	ACTGTTGTAATTTTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	782	
QY	781	CTCGAACCTTAATCCAGACCAAGATTTTCTCAGTTATCTGATGCTCCAGAACTTCCCGTAT	840	
DB	783	CTCGAACCTTAATCCAGACCAAGATTTTCTCAGTTATCTGATGCTCCAGAACTTCCCGTAT	842	
QY	841	ATGAATGATATAAATCTGGGATGAGTATTTTCAGAGAGGCTCAATTCAGGTTTTCATTCCT	900	
DB	843	ATGAATGATATAAATCTGGGATGAGTATTTTCAGAGAGGCTCAATTCAGGTTTTCATTCCT	902	
QY	901	AATAAAGGAGGCTGAAATTTGATCTCTTACCTTTGAACTTGGAGAAATGATTTTGGAGTCC	960	
DB	903	AATAAAGGAGGCTGAAATTTGATCTCTTACCTTTGAACTTGGAGAAATGATTTTGGAGTCC	962	
QY	961	AAACCTCTCATTAAGAAAAAAGGCTGCTGGCAAGAGGAGGAGATGATGAGAAATGC	1020	
DB	963	AAACCTCTCATTAAGAAAAAAGGCTGCTGGCAAGAGGAGGAGATGATGAGAAATGC	1022	



QY 1021 GATTCTCTCAGACATGCTCTTCTTCAAGAGCACCCTTGACTCTCTCCAGAGGAGTTTCA 1080  
 DB 1023 GATTCTCTCAGACATGCTCTTCTTCAAGAGCACCCTTGACTCTCTCCAGAGGAGTTTCA 1082  
 QY 1081 ATTTTCAACAGAGAAAGTAAACACGGGACTTTTAAACAAAGACAAACCAATCTAGCCTTG 1140  
 DB 1083 ATTTTCAACAGAGAAAGTAAACACGGGACTTTTAAACAAAGACAAACCAATCTAGCCTTG 1142  
 QY 1141 GAACAAACCAAGACCCACCAAGTGACAAATGGGACAAATGGACA 1183  
 DB 1143 GAACAAACCAAGACCCACCAAGTGAGGATGGTGCAGATAACA 1185

## RESULT 8

ACA62840  
 ID ACA62840 standard; cDNA; 1485 BP.

AC ACA62840;

XX 01-SEP-2003 (first entry)

XX DE cDNA encoding human kinase.

XX KW human; ss; gene; kinase; gene therapy; cancer; inflammation; psoriasis;  
 KW arteriosclerosis.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

FT 1..2

FT /\*tag= a

FT 3..1193

FT /\*tag= b

FT /product= "Kinase"

FT 1194..1475

FT /\*tag= c

PN US2003027307-A1.

XX PD 06-FEB-2003.

XX PF 06-SEP-2002; 2002US-00254869.

XX PR 09-MAR-2001; 2001US-00801876.

XX PA (APPL-) APPLERA CORP.

XX PI Xie J, Yan C, Di Francesco V, Beasley EM;

XX WP1; 2003-492035/58.

XX PP-PSDB; AB062276.

XX PT New isolated human kinase proteins, useful for treating disorders

XX PT mediated by kinase pathway (e.g. cancers, inflammations, arteriosclerosis

XX PT or psoriasis), or for development of human therapeutics and diagnostic

XX PT compositions.

XX PS Claim 4; Fig 1; 185pp; English.

XX CC The invention relates to a new isolated human kinase peptide. The human  
 CC kinase peptide and nucleic acid molecules are useful in the development  
 CC of human therapeutics and diagnostic compositions. The peptides are  
 CC useful for treating disorders (e.g. cancers, inflammations,  
 CC arteriosclerosis or psoriasis) characterised by an absence of,  
 CC inappropriate, or unwanted expression of the kinase protein. These  
 CC molecules are particularly useful as models for developing human  
 CC therapeutic targets, identifying therapeutic proteins, or serving as  
 CC targets for the development of human therapeutic agents that modulate  
 CC kinase activity in cells and tissues that express the kinase. The  
 CC peptides are also useful for raising antibodies or eliciting an immune  
 CC response; as a reagent (including the labelled reagent) in assays  
 CC designed to quantitatively determine levels of the protein (or its  
 CC binding partner or ligand) in biological fluids; or as markers for

CC tissues in which the corresponding protein is preferentially expressed.  
 CC The agents identified are useful for treating a subject with a disorder  
 CC mediated by kinase pathway. The present sequence represents cDNA encoding  
 CC a human kinase

SQ Sequence 1485 BP; 471 A; 316 C; 331 G; 367 T; 0 U; 0 Other;

Query Match 94.8%; Score 1160.6; DB 8; Length 1485;

Best Local Similarity 98.8%; Pred. No. 0;

Matches 116%; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGGGAGCCCAACACTTCAAGAAAAACCAACAGTGTGTTGATGAAAAATCAAGATGCAACTTT 60

DB 3 ATGGGAGCCCAACACTTCAAGAAAAACCAACAGTGTGTTGATGAAAAATCAAGATGCAACTTT 62

QY 61 GACCACTTTGAAATTTTGGAGCCATTGGGAAAGGCGATTTGGGAAGTCTGCATTTGA 120

DB 63 GACCACTTTGAAATTTTGGAGCCATTGGGAAAGGCGATTTGGGAAGTCTGCATTTGA 122

QY 121 CAGAGAATGATACCAAGAGATGACGAATGAAGTACATGATATAAACAAGTGGCTG 180

DB 123 CAGAGAATGATACCAAGAGATGACGAATGAAGTACATGATATAAACAAGTGGCTG 182

QY 181 GAGCGCAATGAAGTGAAGATGCTTCAAGGAACTCCAGATCATGCAAGGCTCTGGAGCAC 240

DB 183 GAGCGCAATGAAGTGAAGATGCTTCAAGGAACTCCAGATCATGCAAGGCTCTGGAGCAC 242

QY 241 CTTTCTCTGGTTAAATTTGTGTATTCCTTCCAAGATGAGGAAGACATGTTCAFTGGTGGT 300

DB 243 CTTTCTCTGGTTAAATTTGTGTATTCCTTCCAAGATGAGGAAGACATGTTCAFTGGTGGT 302

QY 301 GACCTCTCTGGTGGAGACCTGCTTATCACCCTCAACAGACCTCCACTTCAAGGAA 360

DB 303 GACCTCTCTGGTGGAGACCTGCTTATCACCCTCAACAGACCTCCACTTCAAGGAA 362

QY 361 GAAACAGTGAAGCTCTTCATCTGTGAGCTGGTTCATGCGCCCTGACTACCTGCAGAACCCAG 420

DB 363 GAAACAGTGAAGCTCTTCATCTGTGAGCTGGTTCATGCGCCCTGACTACCTGCAGAACCCAG 422

QY 421 CGCATCATTCACAGGATATGAAGCTTGACATATTTTACTTGCAGAACATGGGCGAGTG 480

DB 423 CGCATCATTCACAGGATATGAAGCTTGACATATTTTACTTGCAGAACATGGGCGAGTG 482

QY 481 CACATCACAGATTTCAACATTCGTGCTGCTGCCAGGAGACACAGATTCACCATG 540

DB 483 CACATCACAGATTTCAACATTCGTGCTGCTGCCAGGAGACACAGATTCACCATG 542

QY 541 GCTGGCACCAAGCTTACATGGCACCTGAGATGTTGAGTCCAGAAAAGGAGCAGGCTAT 600

DB 543 GCTGGCACCAAGCTTACATGGCACCTGAGATGTTGAGTCCAGAAAAGGAGCAGGCTAT 602

QY 601 TCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACTGCTGAGAGGCCGG 660

DB 603 TCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACTGCTGAGAGGCCGG 662

QY 661 AGACGCTGTCATATTCGCTCCAGTACTTCCAGCAAGGAATTTGACACAGTGTGACAG 720

DB 663 AGACGCTGTCATATTCGCTCCAGTACTTCCAGCAAGGAATTTGACACAGTGTGACAG 722

QY 721 ACTGTTGTAACTTACCTTCTGCTGCTGCTCACAGAAATGCTGCTTCTTAAAAAGCTA 780

DB 723 ACTGTTGTAACTTACCTTCTGCTGCTGCTCACAGAAATGCTGCTTCTTAAAAAGCTA 782

QY 781 CTGGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT 840

DB 783 CTGGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT 842

QY 841 ATGATGATATAAATCGGATGAGTGTGTTTTCAGAGAGGCTCATTCAGGTTTCATTCCT 900

DB 843 ATGATGATATAAATCGGATGAGTGTGTTTTCAGAGAGGCTCATTCAGGTTTCATTCCT 902

QY 901 AATAAAGCGAGGCTGAATTTGATGATCCTTACCTTCAACTTCAGGAAATGATTTGGAGTCC 960

DB 901 AATAAAGCGAGGCTGAATTTGATGATCCTTACCTTCAACTTCAGGAAATGATTTGGAGTCC 960

Db 903 AATAAGGCGGCTGAATTTGTGATCTTAACTTGAAGTTCAGGAATGATTTGGATCC 962

QY 961 AAACCTCTACATAAGAAAAAAGCGCTCTGCGAAAGAGAGAGATATGAGAAATGC 1020

Db 963 AAACCTCTACATAAGAAAAAAGCGCTCTGCGAAAGAGAGAGATATGAGAAATGC 1022

QY 1021 GATTTCTTCAGACATGCTCTTCTTAAGAGACCTTGTCTGTCTGTCAGAGAGATTCATA 1080

Db 1023 GATTTCTTCAGACATGCTCTTCTTAAGAGACCTTGTCTGTCTGTCAGAGAGATTCATA 1082

QY 1081 ATTTTTCACAGAGAAAAAGTAAACAGGAGCTTTTAAACAAAAGACCAACCAATCTAGCCTTG 1140

Db 1083 ATTTTTCACAGAGAAAAAGTAAACAGGAGCTTTTAAACAAAAGACCAACCAATCTAGCCTTG 1142

QY 1141 GAAACAAACCAAGACCCACCAAGTGCACAAATGGCAATGGACA 1183

Db 1143 GAAACAAACCAAGACCCACCAAGTGCACAAATGGCAATGGACA 1185

RESULT 9

AA06704

AA06704 standard; cDNA; 981 BP.

AA06704;

12-SEP-2001 (first entry)

Polynucleotide sequence encoding human protein kinase #4.

Human; protein kinase; PK; STK; cancer; cardiovascular disease;

metabolic disorder; immune related disease; neurological disorder;

neurodegenerative disorder; inflammatory disorder; infectious disease;

reproductive disorder; gene therapy; ss.

Homo sapiens.

W0200138503-A2.

31-MAY-2001.

22-NOV-2000; 2000MO-US032085.

24-NOV-1999; 99US-0167482P.

(SUGEN-) SUGEN INC.

Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R,

Flanagan P, Clary D;

WPI; 2001-343950/36.

P-PSDB; AAU03504.

Nucleic acids encoding human kinase polypeptides, useful for preventing

diagnosing and/or treating e.g. cancer, immune, cardiovascular and

neural-associated diseases, and microbial infections.

Example 1; Fig 1; 433pp; English.

AA06701-AA06757 encode for novel human protein kinases #1-57. The novel

protein kinases have been identified as members of the tyrosine or

serine/threonine kinase (PTK and STK) families. The polynucleotides

encoding protein kinases and the polypeptides may be used in the

prevention, diagnosis and treatment of diseases associated with

inappropriate kinase expression. For example, they may be used to treat

cancers (especially cancers of haematopoietic origin), cardiovascular

disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),

immune related diseases (e.g. rheumatoid arthritis), neurological

disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.

Parkinson's disease), inflammatory disorders (e.g. asthma), infectious

disease (e.g. HIV) and reproductive disorders (e.g. infertility).

Additionally, polynucleotides encoding protein kinases may be used for

gene therapy and as DNA probes in diagnostic assays. The protein kinase

polypeptides may be used as antigens in the production of antibodies

CC against the protein kinases and in assays to identify modulators of

protein kinase expression and activity

XX

SQ Sequence 981 BP; 294 A; 207 C; 245 G; 235 T; 0 U; 0 Other;

Query Match 68.0%; Score 832.8; DB 4; Length 981;

Best Local Similarity 90.8%; Pred. No. 3.4e-232;

Matches 904; Conservative 0; Mismatches 77; Indels 15; Gaps 1;

QY 1 ATGGGAGCCCAACACTTCAAGAAACCCACAGTGTGTGATGAAATGAAGATCTCACTTT 60

Db 1 ATGGGAGCCCAACACTTCAAGAAACCCACAGTGTGTGATGAAATGAAGATCTCACTTT 60

QY 61 GACCACTTTGAAATTTTGGAGCCATTTGGAAAGCGAGTTTGGAGAGTCTGCAATGTA 120

Db 61 GACCACTTTGAAATTTTGGAGCCATTTGGAAAGCGAGTTTGGAGAGTCTGCAATGTA 120

QY 121 CAGAAGATGATACCAAGAGATGTACGCAATGAAGTACATGAATAAAACAAAGTCCCTG 180

Db 121 CAGAAGATGATACCAAGAGATGTACGCAATGAAGTACATGAATAAAACAAAGTCCCTG 180

QY 181 GAGCGCAATGAAGTGAAGAAATGCTTCAAGAACTCCAGATCATGCGAGTCTGAGACAC 240

Db 181 GAGCGCAATGAAGTGAAGAAATGCTTCAAGAACTCCAGATCATGCGAGTCTGAGACAC 240

QY 241 CCTTCTCTGTTAATTTGTGTTATTCCTTCCAGATGAGAGACATGTTCTGTTGGTG 300

Db 241 CCTTCTCTGTTAATTTGTGTTATTCCTTCCAGATGAGAGACATGTTCTGTTGGTG 300

QY 301 GACCTCTCTGCTGGTGAGACCTGCGTTATCACCTGCAACAGAACTCCACTTCAAGGAA 360

Db 301 GACCTCTCTGCTGGTGAGACCTGCGTTATCACCTGCAACAGAACTCCACTTCAAGGAA 360

QY 361 GAAACAGTGAAGCTCTTCACTGTGAGTGTGTCATGCGCCCTGGAATACCTGCGAGACCAG 420

Db 361 GAAACAGTGAAGCTCTTCACTGTGAGTGTGTCATGCGCCCTGGAATACCTGCGAGACCAG 420

QY 421 CGCATCATTTACAGGGATATGAAGCTGACATATTTTACTTACCAACATGCGGACCTG 480

Db 421 CGCATCATTTACAGGGATATGAAGCTGACATATTTTACTTACCAACATGCGGACCTG 480

QY 481 CACATCACAGATTTCAACATTTGCGATGCTGCCAGGAGAGACACAGATTACCACTG 540

Db 481 CACATCACAGATTTCAACATTTGCGATGCTGCCAGGAGAGACACAGATTACCACTG 540

QY 541 GTTGGCAACCAAGCTTTACATGTCAGTGTGTCATGCTCCAGTCCAGAAAGAGAGCTAT 600

Db 541 GTTGGCAACCAAGCTTTACATGTCAGTGTGTCATGCTCCAGTCCAGAAAGAGAGCTAT 600

QY 601 TCCCTTTGCTGTGACTGTGCTCCCTGGGAGTGCAGGATATGAACTGCTGAGAGCCGG 660

Db 601 TCCCTTTGCTGTGACTGTGCTCCCTGGGAGTGCAGGATATGAACTGCTGAGAGCCGG 660

QY 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACAGTTTGAGAG 720

Db 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACAGTTTGAGAG 720

QY 721 ACTGTTGTAACCTTACCTTCTGCTGCTGTCACAGGAATGCTGTCATCTTAAAGAGTA 780

Db 721 ACTGTTGTAACCTTACCTTCTGCTGCTGTCACAGGAATGCTGTCATCTTAAAGAGTA 780

QY 781 CTCGAACTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT 840

Db 781 CTCGAACTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT 840

QY 841 ATGAATGATATAAATCTGGGATGCGATGTTTTCAGAGAGGCTCATTCAGGTTTCATTCCT 900

Db 841 ATGAATGATATAAATCTGGGATGCGATGTTTTCAGAGAGGCTCATTCAGGTTTCATTCCT 900

QY 901 AATAAGGCGGCTGAATTTGTGATCTTAACTTGAAGTTCAGGAATGATTTGGATCC 960

Db 901 AATAAGGCGGCTGAATTTGTGATCTTAACTTGAAGTTCAGGAATGATTTGGATCC 960

QY 961 AATAAGGCGGCTGAATTTGTGATCTTAACTTGAAGTTCAGGAATGATTTGGATCC 962

Db 961 AATAAGGCGGCTGAATTTGTGATCTTAACTTGAAGTTCAGGAATGATTTGGATCC 962

QY 961 AAACCTCTACATGACAAAAAAGCGTCTGCAAG 996  
 Db 946 AAACCTCTACATGACAAAAAAGCGTCTGCAAG 981

RESULT 10  
 ABA08463  
 ID ABA08463 standard; cDNA; 678 BP.  
 XX AC ABA08463;  
 XX DT 11-JAN-2002 (first entry)  
 XX DE Human Ser/Thr kinase homologue-encoding cDNA, SEQ ID NO:239.  
 XX KW Human; cytokine; cell proliferation; cell differentiation; growth factor;  
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;  
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;  
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;  
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;  
 KW chronic inflammatory condition; proliferative retinopathy;  
 KW atherosclerosis; coronary heart disease; arterial ischaemia;  
 KW bone disorder; osteoporosis; vascular growth disorder;  
 KW tissue regeneration; wound healing; infection; immune disorder;  
 KW cell culture; drug screening; gene therapy; antiinflammatory;  
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;  
 KW cytosstatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;  
 KW antifungal; vulnery; antiulcer; ss.  
 XX OS Homo sapiens.  
 XX PN WO200157188-A2.  
 XX PE 09-AUG-2001.  
 XX PF 05-FEB-2001; 2001WO-US003800.  
 XX PR 03-FEB-2000; 2000US-00496914.  
 XX PS 27-APR-2000; 2000US-00560875.  
 XX PA (HYSE-) HYSEQ INC.  
 XX PI Tang YT, Liu C, Drmanac RT;  
 XX WPI; 2001-457740/49.  
 XX DR P-PSDB; ABB11219.  
 XX PT Human proteins and DNA encoding sequences useful for preventing, treating  
 XX or ameliorating a medical condition in a mammalian subject e.g. arthritis  
 XX and cancer.  
 XX PS Claim 1; Page 422; 1963pp; English.

CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and  
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The  
 CC invention also relates to vectors and recombinant host cells comprising a  
 CC nucleotide of the invention, methods of producing the novel polypeptides,  
 CC antibodies against the polypeptides, methods of detecting the nucleotides  
 CC or polypeptides in a sample, and methods of identifying compounds which  
 CC bind to polypeptides of the invention. Although novel, many of the  
 CC polypeptides of the invention have homology to known proteins, thereby  
 CC giving an insight into their probable biological activities, and hence  
 CC potential therapeutic applications. The polypeptides of the invention may  
 CC have various activities, including cytokine, cell proliferation or cell  
 CC differentiation activities; stem cell growth factor activity;  
 CC haematopoiesis regulatory activity; tissue growth activity;  
 CC immunomodulatory activity; activin- or inhibin-related activities;  
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or  
 CC thrombolytic activities; receptor or ligand activities; or may be  
 CC involved in oncogenesis, cancer cell proliferation or metastasis.  
 CC depending on their biological activities, polypeptides and nucleotides of  
 CC the invention are useful for preventing, treating or ameliorating medical  
 CC conditions, e.g., by protein or gene therapy. Such conditions include

CC cancers, haematopoietic disorders (e.g. myeloid or lymphoid cell  
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),  
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,  
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal  
 CC vascular growth. Polypeptides involved with tissue regeneration and  
 CC repair (or nucleic acids encoding them) may be used to promote wound  
 CC healing (e.g., of burns, incisions and ulcers), while those with  
 CC immunomodulatory activities may be used in the treatment of viral,  
 CC bacterial and fungal infections in addition to immune disorders.  
 CC Polypeptides with growth factor activity may be used in cell cultures to  
 CC promote cell growth. For example, such polypeptides may be used to  
 CC manipulate stem cells in culture to give rise to neuroepithelial cells  
 CC that can be used to augment or replace cells damaged by illness,  
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides  
 CC may also be used in the diagnosis of the above conditions, and in drug  
 CC screening techniques. The present sequence represents a cDNA encoding a  
 CC novel human polypeptide of the invention  
 XX  
 SQ Sequence: 678 BP; 203 A; 148 C; 152 G; 175 T; 0 U; 0 Other;

Query Match 55.0%; Score 672.8; DB 4; Length 678;  
 Best Local Similarity 99.7%; Pred. No. 1.4e-185;  
 Matches 674; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 435 ATGAAGCCTGACATATTTTACTTGCAGAAATGGGACGTCACATCAGATTTCAAC 498  
 Db 1 ATGAAGCCTGACATATTTTACTTGCAGAAATGGGACGTCACATCAGATTTCAAC 60  
 QY 495 ATTGCTCGATGCTGCCAGGAGACACAGATTTACCATGGCTGGCCACCAAGCTTAC 558  
 Db 61 ATTGCTCGATGCTGCCAGGAGACACAGATTTACCATGGCTGGCCACCAAGCTTAC 120  
 QY 555 ATGGCACCCTGAGATGTTTCAGCTCCAGAAAAGGAGCAGCTATTCCTTTGCTGTGACTGG 618  
 Db 121 ATGGCACCCTGAGATGTTTCAGCTCCAGAAAAGGAGCAGCTATTCCTTTGCTGTGACTGG 180  
 QY 615 TGGTCCCTGGGAGTGACGGCATATGAACTGCTGAGAGCCGAGACCGTATCATATTCCG 678  
 Db 181 TGGTCCCTGGGAGTGACGGCATATGAACTGCTGAGAGCCGAGACCGTATCATATTCCG 240  
 QY 675 TCCAGTACTTCCAGCAAGGAATGTACACAGTTTGAGACGACTGTTGTAACCTTACCCT 738  
 Db 241 TCCAGTACTTCCAGCAAGGAATGTACACAGTTTGAGACGACTGTTGTAACCTTACCCT 300  
 QY 735 TCTGCTGCTGTCACAGGAATGGTGTCTCACTTCTTAAAAAGCTACTCGAACCTTAATCCAGAC 798  
 Db 301 TCTGCTGCTGTCACAGGAATGGTGTCTCACTTCTTAAAAAGCTACTCGAACCTTAATCCAGAC 360  
 QY 795 CAACGATTTTCTAGTATCTGATGTCAGACTTCCGATATATGAATGATATTAACCTGG 858  
 Db 361 CAACGATTTTCTAGTATCTGATGTCAGACTTCCGATATATGAATGATATTAACCTGG 420  
 QY 855 GATCAGTTTTTTCAGAGAGGCTCAATTCAGGTTTCAATTCCTTAAGGAGGAGCTGAAT 918  
 Db 421 GATCAGTTTTTTCAGAGAGGCTCAATTCAGGTTTCAATTCCTTAAGGAGGAGCTGAAT 480  
 QY 915 TGTGATCCTTACCTTTGAACTTGAGGAATGATTTTGGAGTCCAAACCTCTACATPAAGAAA 978  
 Db 481 TGTGATCCTTACCTTTGAACTTGAGGAATGATTTTGGAGTCCAAACCTCTACATPAAGAAA 540  
 QY 975 AAAAGGCTCTGGCAAGAGAGAGAGATATGAGGAATGCGATTTCTTCCAGACATGT 1038  
 Db 541 AAAAGGCTCTGGCAAGAGAGAGAGATATGAGGAATGCGATTTCTTCCAGACATGT 600  
 QY 1035 CTTCCTTCAAGAGACCTTGTACTCTGTCCAGAGAGGATTCATATTTTCAACAGAGAAAAA 1098  
 Db 601 CTTCCTTCAAGAGACCTTGTACTCTGTCCAGAGAGGATTCATATTTCAACAGAGAAAAA 660  
 QY 1099 GTAAACAGGAGCTTTA 1114  
 Db 661 GTAAACAGGAGCTGTA 676

RESULT 11  
 AAD23677  
 ID AAD23677 standard; cDNA; 711 BP.  
 XX  
 AC AAD23677;  
 XX  
 DT 07-MAR-2002 (first entry)  
 XX  
 DE Novel human protein (NHP) kinase cDNA #2.  
 XX  
 KW Novel human protein; NHP; gene therapy; diagnosis; drug screening;  
 KW gene expression; breast cancer; prostate cancer; nutraceutical; cosmetic;  
 KW medical disorder; mental; biological; physiological; chemotherapeutic;  
 KW ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 XX CDS 1..711  
 XX /\*tag= a  
 XX /product= "Novel human protein (NHP) kinase"  
 XX  
 XX WO200181557-A2.  
 XX  
 XX 01-NOV-2001.  
 XX  
 XX 24-APR-2001; 2001WO-US013149.  
 XX  
 XX 25-APR-2000; 2000US-0199499P.  
 XX  
 XX (LEXI-) LEXICON GENETICS INC.  
 XX  
 XX Hu Y, Nepomnichy B, Wang X, Donoho G, Scoville J, Walke DW;  
 XX WPI: 2002-034442/04.  
 XX P-PSDB; AAE14259.  
 XX  
 XX New nucleic acid molecules encoding new human proteins, useful in  
 XX diagnosis, drug screening, clinical trial monitoring, treatment of  
 XX physiological disorders, and cosmetic or nutraceutical applications.  
 XX  
 XX Disclosure; Page 40; 44pp; English.  
 XX  
 XX The invention relates to novel human protein (NHP) kinases and their  
 XX corresponding cDNA molecules. NHP kinase and its DNA are useful as  
 XX reagents in assays for screening compounds that can be used as  
 XX pharmaceutical reagents useful in the therapeutic treatment of mental,  
 XX biological and medical disorders, and also as chemotherapeutic agents  
 XX useful in the treatment of breast cancer and prostate cancer. NHP DNA is  
 XX useful for diagnosis, drug screening, clinical trial monitoring, the  
 XX treatment of physiological disorders or diseases, and cosmetic and  
 XX nutraceutical applications. NHP DNA is also useful for the identification  
 XX of coding sequence and the mapping of a unique gene to a particular  
 XX chromosome. NHP DNA is further useful as hybridization probes for  
 XX screening libraries and assessing gene expression patterns, and also for  
 XX the detection of mutant NHPs or inappropriately expressed NHPs for  
 XX disease diagnosis. NHP DNA is also useful in gene therapy. The present  
 XX sequence is novel human protein (NHP) kinase cDNA which is similar to  
 XX serine/threonine protein kinases, ribosomal protein kinases and CAMP-  
 XX dependent kinases cDNA related to the invention  
 XX  
 XX Sequence 711 BP; 199 A; 153 C; 181 G; 178 T; 0 U; 0 Other;  
 XX  
 XX Query Match 54.0%; Score 661; DB 6; Length 711;  
 XX Best Local Similarity 100.0%; Pred. No. 4.1e-182;  
 XX Matches 661; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 1 ATGGGAGCCAACTTCAAGAAACCAACCACTGTTTGTATGAAATGAAGATGTCACACTTT 60  
 XX  
 XX 1 ATGGGAGCCAACTTCAAGAAACCAACCACTGTTTGTATGAAATGAAGATGTCACACTTT 60  
 XX  
 XX 61 GACCACTTTGAATTTTGGAGCCATTGGGAAGGACAGTTTGGGAGGCTCTGATTTGA 120

Db 61 GACCACTTTGAATTTTGGAGCCATTGGGAAGGACAGTTTGGGAGGCTCTGATTTGA 120  
 QY 121 CAGAAAGATGATACCAAGAAGATGTACGCAATGAAGTACATGAATAAACAAGTSCGTG 180  
 Db 121 CAGAAAGATGATACCAAGAAGATGTACGCAATGAAGTACATGAATAAACAAGTSCGTG 180  
 QY 181 GAGCGCAATGAAGTGAAGAAATGTCTTCAAGNACTCCAGATCATCGAGGCTCGAGAC 240  
 Db 181 GAGCGCAATGAAGTGAAGAAATGTCTTCAAGNACTCCAGATCATCGAGGCTCGAGAC 240  
 QY 241 CCTTTCTCTGTTAAATTTGGGTATTCTTCCAAAGATGAGGAAGACATGTTCAATGGTGTG 300  
 Db 241 CCTTTCTCTGTTAAATTTGGGTATTCTTCCAAAGATGAGGAAGACATGTTCAATGGTGTG 300  
 QY 301 GACCTCCTGCTGGGTGAGACCTGCTTATACCTGCAACAGACGCTCCACTTCAAGGAA 360  
 Db 301 GACCTCCTGCTGGGTGAGACCTGCTTATACCTGCAACAGACGCTCCACTTCAAGGAA 360  
 QY 361 GAAACAGTGAAGCTCTTCAATCTGAGCTGGTGTGCTGAGTACCTGAGAACCCAG 420  
 Db 361 GAAACAGTGAAGCTCTTCAATCTGAGCTGGTGTGCTGAGTACCTGAGAACCCAG 420  
 QY 421 CGCATCATTCAAGGATATGAAGCTGACATATTTTACTTGACGAAACATGGGACCGTG 480  
 Db 421 CGCATCATTCAAGGATATGAAGCTGACATATTTTACTTGACGAAACATGGGACCGTG 480  
 QY 481 CACATCACAGATTTCAACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
 Db 481 CACATCACAGATTTCAACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
 QY 541 GCTGGCACCAGCCCTTACATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
 Db 541 GCTGGCACCAGCCCTTACATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
 QY 601 TCTTTTCTGTTGACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
 Db 601 TCTTTTCTGTTGACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
 QY 661 A 661  
 Db 661 A 661

RESULT 12  
 AAD23676  
 ID AAD23676 standard; cDNA; 678 BP.  
 XX  
 AC AAD23676;  
 XX  
 DT 07-MAR-2002 (first entry)  
 XX  
 DE Novel human protein (NHP) kinase cDNA #1.  
 XX  
 KW Novel human protein; NHP; gene therapy; diagnosis; drug screening;  
 KW gene expression; breast cancer; prostate cancer; nutraceutical; cosmetic;  
 KW medical disorder; mental; biological; physiological; chemotherapeutic;  
 KW ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 XX CDS 1..678  
 XX /\*tag= a  
 XX /product= "Novel human protein (NHP) kinase"  
 XX  
 XX WO200181557-A2.  
 XX  
 XX 01-NOV-2001.  
 XX  
 XX 24-APR-2001; 2001WO-US013149.  
 XX  
 XX 25-APR-2000; 2000US-0199499P.

PR 01-MAY-2000; 2000US-0201227P.  
 PA (LEXI-) LEXICON GENETICS INC.  
 XX Hu Y, Nepomnichy B, Wang X, Donoho G, Scoville J, Walke DW;  
 XX MPI: 2002-034442/04.  
 DR P-PSDB; AME14258.  
 XX  
 PT New nucleic acid molecules encoding new human proteins, useful in  
 PT diagnosis, drug screening, clinical trial monitoring, treatment of  
 PT physiological disorders, and cosmetic or nutraceutical applications.  
 XX Disclosure; Page 39; 44pp; English.  
 XX  
 CC The invention relates to novel human protein (NHP) kinases and their  
 CC corresponding cDNA molecules. NHP kinase and its DNA are useful as  
 CC reagents in assays for screening compounds that can be used as  
 CC pharmaceutical reagents useful in the therapeutic treatment of mental,  
 CC biological and medical disorders, and also as chemotherapeutic agents  
 CC useful in the treatment of breast cancer and prostate cancer. NHP DNA is  
 CC useful for diagnosis, drug screening, clinical trial monitoring, the  
 CC treatment of physiological disorders or diseases, and cosmetic and  
 CC nutraceutical applications. NHP DNA is also useful for the identification  
 CC of coding sequence and the mapping of a unique gene to a particular  
 CC chromosome. NHP DNA is further useful as hybridisation probes for  
 CC screening libraries and assessing gene expression patterns, and also for  
 CC the detection of mutant NHPs or inappropriately expressed NHPs for  
 CC disease diagnosis. NHP DNA is also useful in gene therapy. The present  
 CC sequence is novel human protein (NHP) kinase cDNA which is similar to  
 CC serine/threonine protein kinases, ribosomal protein kinases and CAMP-  
 CC dependent kinases cDNA related to the invention  
 XX  
 SQ Sequence 678 BP; 195 A; 148 C; 179 G; 156 T; 0 U; 0 Other;  
 XX  
 Query Match 53.9%; Score 660; DB 6; Length 678;  
 Best Local Similarity 100.0%; Pred. No. 7.7e-182;  
 Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 ATGGGAGCAACACCTTCAAGAAACCCACGAGTGTGATGAAATGAAGATGCAACTTT 60  
 DB 1 ATGGGAGCAACACCTTCAAGAAACCCACGAGTGTGATGAAATGAAGATGCAACTTT 60  
 OY 61 GACCACTTTGAAATTTCCGAGCCATTCGGAAAGCAGCTTTTGGGAAGCTGCAATTGTA 120  
 DB 61 GACCACTTTGAAATTTCCGAGCCATTCGGAAAGCAGCTTTTGGGAAGCTGCAATTGTA 120  
 OY 121 CAGAAGATGATACCAAGAGATGTACGCAATGAAGTACATGAATAACAAAGTCGTG 180  
 DB 121 CAGAAGATGATACCAAGAGATGTACGCAATGAAGTACATGAATAACAAAGTCGTG 180  
 OY 181 GAGCGCAATGAAGTGAGAAATGCTCTTCAAGGAATCCAGATCATGCGGGTCTGAGCAC 240  
 DB 181 GAGCGCAATGAAGTGAGAAATGCTCTTCAAGGAATCCAGATCATGCGGGTCTGAGCAC 240  
 OY 241 CCTTTCCTGGTAAATTTGGTATTCCTTCAAGATGAGGAGACATGTTATGTTGGTGTG 300  
 DB 241 CCTTTCCTGGTAAATTTGGTATTCCTTCAAGATGAGGAGACATGTTATGTTGGTGTG 300  
 OY 301 GACCTCTGCTGGTGGAGACTGCTGTTATCCTCCAGCAACAGACGTCCTCAAGGAA 360  
 DB 301 GACCTCTGCTGGTGGAGACTGCTGTTATCCTCCAGCAACAGACGTCCTCAAGGAA 360  
 OY 361 GAAACAGTGAAGCTCTTCACTGTGAGCTGGTGTGATGGCCCTGGACTCTCAGAACCCAG 420  
 DB 361 GAAACAGTGAAGCTCTTCACTGTGAGCTGGTGTGATGGCCCTGGACTCTCAGAACCCAG 420  
 OY 421 CGCATCATTCAGGGATATGAGCCTGACAAATATTTTACTTGGACAAATGGGACGCTG 480  
 DB 421 CGCATCATTCAGGGATATGAGCCTGACAAATATTTTACTTGGACAAATGGGACGCTG 480  
 OY 481 CACATCACAGATTTCAACATGCTGCGATGTGCCCGGAGACACAGATTAACCAACCATG 540  
 DB 481 CACATCACAGATTTCAACATGCTGCGATGTGCCCGGAGACACAGATTAACCAACCATG 540

DB 481 CACATCACAGATTTCAACATGCTGCGATGTGCCCGGAGACACAGATTAACCAACCATG 540  
 OY 541 GCTGSCACCAAGCCTTACATGCGACCTGAGATGTTTCACTCCAGAAAAGGAGCAGCTAT 600  
 DB 541 GCTGSCACCAAGCCTTACATGCGACCTGAGATGTTTCACTCCAGAAAAGGAGCAGCTAT 600  
 OY 601 TCCCTTGTCTGTTGACTGTTGCTGCTGCGAGTACGGCATATGAATGCTGCTGAGAGCCGG 660  
 DB 601 TCCCTTGTCTGTTGACTGTTGCTGCTGCGAGTACGGCATATGAATGCTGCTGAGAGCCGG 660  
 XX  
 RESULT 13  
 ABQ61051  
 ID ABQ61051 standard; cDNA; 1587 BP.  
 XX  
 AC ABQ61051;  
 XX  
 DT 26-FEB-2003 (first entry)  
 XX  
 DE Serine/threonine kinase encoding sequence.  
 XX  
 KW Neuroprotective; immunomodulator; cancer; chromosome 4p16.1-p14;  
 KW cytoskeletal; anti-inflammatory; gene therapy; nutritional supplement;  
 KW wound; burn; ulcer; Alzheimer's disease; Huntington's disease;  
 KW amyotrophic lateral sclerosis; autoimmune disorder; inflammation;  
 KW vulnery; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200231111-A2.  
 XX  
 PD 18-APR-2002.  
 XX  
 PF 11-OCT-2001; 2001WO-US027760.  
 XX  
 PR 12-OCT-2000; 2000US-00687527.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;  
 PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;  
 XX  
 DR MPI; 2002-426278/45.  
 DR N-PSDB; ABP43807.  
 XX  
 PT New polypeptides and their encoded proteins, useful as nutritional  
 PT sources or supplements, or in gene therapy, particularly for treating  
 PT wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or  
 PT inflammation.  
 XX  
 PS Claim 1; SEQ ID # 264; 357pp + Sequence Listing; English.  
 XX  
 CC The invention relates to 446 newly isolated polynucleotide sequences. The  
 CC activity of polynucleotides of the invention may be described as,  
 CC vulnery, neuroprotective, immunomodulator, cytoskeletal and anti-  
 CC inflammatory. Compositions comprising nucleic acids of the invention are  
 CC useful for treating a mammalian subject, or as nutritional sources or  
 CC supplements. These are useful in gene therapy, particularly for treating  
 CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,  
 CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or  
 CC inflammation. The nucleic acids and polypeptides are also useful in  
 CC diagnostic and research methods. The sequences given in records ABQ60788-  
 CC ABQ61233 represent polynucleotides of the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 1587 BP; 414 A; 421 C; 425 G; 327 T; 0 U; 0 Other;  
 XX  
 Query Match 44.3%; Score 542.4; DB 6; Length 1587;  
 Best Local Similarity 69.1%; Pred. No. 2.6e-147;  
 Matches 773; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

QY 1 ATGGGAGCCCAACACTTTCAGAAACACCAAGTGTGTTTATGAAATGAAGATGTCACACTTT 60  
 Db 1 ATGGGCGGAAACCACTCCACAAAGCCCGTGTGTTGACGAGATGAGGAAGTCAACTTT 60  
 QY 61 GACCACCTTGAATTTTGGAGCCATTTGGAAAGGAGTTTGGGAGGCTGCTGATTGTA 120  
 Db 61 GACCATTTTCAGATTCTGGGGCCATTGTTGTAAGGGAGTTTGGAAAGGATGATCATCGTG 120  
 QY 121 CAGAAGATGATACCAAGAGATGTACGCAATGAAGTACATGAATATAAACAAGAGTCCGTG 180  
 Db 121 CAGAGCGAGACACTAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 180  
 QY 181 GAGCGCAATGAAGTGAATATGTTTCAAGAACTCCAGATCATGAGGCTGTGGAGCAC 240  
 Db 181 GAGAGGATGAGGTTGGAATGTTTCCGGAGCTGCAGATCATGCAAGGGCTGTGGAGCAC 240  
 QY 241 CCTTCTGTTTAAATTTGTTGTTTCTTCCAGATGAGGAGACATGTTCAAGTGGTG 300  
 Db 241 CCTTCTGTTTAAATTTGTTGTTTCTTCCAGATGAGGAGACATGTTCAAGTGGTG 300  
 QY 301 GACCTCTGCTGGGTGAGACCTGCGTTATCACTGCAACAGAACGTCACATTTCAAGGAA 360  
 Db 301 GACCTGCTCTGGAGCGACCTGGCTACCATCTGCAGCAGATGTGCAATTTACAGAG 360  
 QY 361 GAAACAGTGAAGCTTTCATCTGTGAGCTGGTCAATGCGCTGACATCTGTGAGAACG 420  
 Db 361 GGGACTGTGAAACTCTACATCTGTGAGCTGGCTGCGCTGAGATCTTTCAGAGTAC 420  
 QY 421 CGCATATTCACAGGATATGAGGCTGACCAATATTTTACTTCAGCAACATGCGCAGTG 480  
 Db 421 CATATTCACAGAGACATCAAGCCAGCAATATCTGCTGATGATGATGATGATGATG 480  
 QY 481 CACATCAGATTTTCAACATTTGCTGATGCTGCTGCCAGGAGACACAGATTACCAATG 540  
 Db 481 CACATCAGACTTCAACATGAGCGGTAGTGAAGAGCAGAAAGGGCTTCTCTCCATG 540  
 QY 541 GCTGGACCAAGCCTTACATGAGGACCTGAGATGTC-----AGCTCCAGAAAGGAC 594  
 Db 541 GCTGGACCAAGCCTTACATGAGGACCTGAGATGTC-----AGCTCCAGAAAGGAC 600  
 QY 595 GGTATTTCTTGTGTTGACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 654  
 Db 601 GGTATTTCTTGTGTTGACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
 QY 655 GGGCGAGACGCTATCATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 714  
 Db 661 GGGCGAGACGCTATCATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
 QY 715 GAGACGATGTTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 774  
 Db 721 AAGGTGGAGCGTGTCCACTACTCTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
 QY 775 AAGTCTATCGAACTAATTCAGACCAACGATTTTCTCAGTTATCTGATGCTCAGAACT 834  
 Db 781 AAGTCTATCGAACTAATTCAGACCAACGATTTTCTCAGTTATCTGATGCTCAGAACT 840  
 QY 835 CCGTATATGATGATATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 894  
 Db 841 CCGTATATGATGATATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 900  
 QY 895 ATTCTATTAAGCAGGCTGAATTTGATGCTTACCTTTGACCTTTGAGGAAATGATTTG 954  
 Db 901 GTGCCCAATAAAGGAGGTGTAATTTGATGCTTACCTTTGACCTTTGAGGAAATGATTT 960  
 QY 955 GAGTCCCAACCTCTACATAAGAAAAAAGGCTGTGCAAGAA-----GGAGAAAGATATG 1011  
 Db 961 GAATCCAAAGCCATTCACAAAAGAGAGAGGATTTGGCAAGACAGATCCAGGATGGC 1020  
 QY 1012 AGGAAATGCGATTTCTTTCAGACATGTTCTTCTTCAAGAGCACTTGTGCTCCAGAG 1071  
 Db 1021 ACAAAGGACAGTGCCTGCTGAATGGAACACCTGCTGAGCACTGTTTGGAGACTGTCCGGAG 1080  
 QY 1072 GAGTTCAATAATTTTCAACAGAGAAAGTAAACAGGGA 1109

Db 1081 GAATTCATCATATTACACAGAGAGGCTCAGAGGCA 1118  
 RESULT 14  
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 ID AAF44625 standard; cDNA; 3224 BP.  
 XX AAF44625;  
 AC AAF44625;  
 DT 27-MAR-2001 (first entry)  
 XX  
 DE Novel protein kinase cDNA, SEQ ID NO: 4.  
 XX  
 KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;  
 immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;  
 dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;  
 immune disorder; cardiovascular disease; neurodegenerative disease;  
 cancer; autoimmune disorder; stroke; inflammatory bowel disease;  
 inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WC200073469-A2.  
 XX  
 PD 07-DEC-2000.  
 XX  
 PF 26-MAY-2000; 2000WO-US014842.  
 XX  
 PR 28-MAY-1999; 99US-0136503P.  
 XX  
 PA (SUBG-) SUGEN INC.  
 XX  
 PI Plowman GD, Martinez R, Whyte D, Sudersanam S;  
 XX WPI: 2001-032161/04.  
 DR P-PSDB; AAB65600.  
 XX  
 PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and  
 PT treating immune-related diseases and disorders, cardiovascular disease,  
 XX neurodegenerative diseases and/or cancers.  
 PS Example 1; Fig 2; 310pp; English.  
 XX  
 CC The present sequence encodes a novel protein kinase. The nucleic acids  
 and the protein kinases they encode may be used in the treatment and  
 CC diagnosis of diseases associated with inappropriate kinase expression  
 CC such as immune-related diseases and disorders, cardiovascular disease,  
 CC neurodegenerative diseases and/or cancers. The nucleic acids and  
 CC complementary sequences may also be used as DNA probes in diagnostic  
 CC assays. The kinase polypeptides may be used as antigens in the production  
 CC of antibodies of kinase expression and activity. Anti-kinase antibodies  
 CC and kinase antagonists may also be used to down regulate kinase  
 CC expression and activity. Diseases related to kinase expression and  
 CC activity include rheumatoid arthritis, atherosclerosis, autoimmune  
 CC disorders, complications of organ transplantation, myocardial infarction,  
 CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative  
 CC stress related disorders, chronic inflammatory bowel disease, chronic  
 CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,  
 CC psoriasis, rhinitis, autoimmune, diabetes, cancers and reproductive  
 CC disorders  
 XX  
 SQ Sequence 3224 BP; 820 A; 812 C; 769 G; 823 T; 0 U; 0 Other;  
 Query Match 44.3%; Score 542.4; DB 4; Length 3224;  
 Best Local Similarity 69.1%; Pred. No. 3.9e-147;  
 Matches 773; Conservative 0; Mismatches 336; Indels 9; Gaps 2;  
 QY 1 ATGGGAGCCCAACACTTTCAGAAACACCAAGTGTGTTTATGAAATGAAGATGTCACACTTT 60  
 Db 65 ATGGGCGGAAACCACTCCACAAAGCCCGTGTGTTGACGAGATGAGGAAGTCAACTTT 124  
 QY 61 GACCACCTTGAATTTTGGAGCCATTTGGAAAGGAGTTTGGGAGGCTGCTGATTGTA 120

ADA19317	ADA19317 standard; cDNA; 3224 BP.
XX	
XX	ADA19317;
XX	
XX	
DT	20-NOV-2003 (first entry)
XX	
DE	Human insulin resistance marker IRM210 (Ser/Thr protein kinase) cDNA #2.
XX	
XX	Insulin resistance; IR; susceptibility; diagnosis;
KW	insulin resistance marker; IRM; polymorphism; genotype; hypertension;
KW	diyslipidemia; type 2 diabetes; obesity; coronary artery disease;
KW	drug screening; antidiabetic; cardiant; antilipaeamic; hypotensive; human;
KW	gene; ss.
XX	
XX	
OS	Homo sapiens.
XX	
XX	WO200298355-A2.
XX	
XX	12-DEC-2002.
XX	
PF	03-JUN-2002; 2002WO-US017227.
PF	
XX	01-JUN-2001; 2001US-0295264P.
PP	
XX	(CLIN-) CLINGENIX INC.
PA	
XX	
XX	Ma Y, Lih C, Chen F, Fairman J, Chen YI;
PI	
XX	WPI: 2003-148601/14.
XX	
DR	

Diagnosing for insulin resistance (IR) an IR-related condition, e.g. hypertension, diabetes or obesity, comprises detecting an altered or difference in expression of insulin resistance marker (IRM) genes in a sample from the subject.

Claim 1: Page: 125pp: English.

The invention relates to a method for diagnosing insulin resistance (IR), an IR-related condition, or susceptibility to IR or an IR-related condition in a patient. The method comprises detecting a difference in expression of at least one insulin resistance marker (IRM) in a biological sample from the patient, compared to the level of expression of the IRM in reference individuals who are not insulin resistant. The invention also encompasses screening for an agent to determine its usefulness in treating IR; the identification of a polymorphism associated with an IR phenotype or risk of developing IR; estimating the frequency of a haplotype for a set of nucleotide polymorphism markers in a population; detecting an association between a haplotype and a phenotype; and identifying genes associated with a disease state. The methods of the invention are useful for diagnosing insulin resistance (IR), an IR-related condition, or susceptibility to IR or an IR-related condition. Such conditions include hypertension, dyslipidaemia, type 2 diabetes, obesity or coronary artery disease. The methods are also useful in screening for agents useful in the treatment of these disorders. The present sequence represents an IRM cDNA which is specifically claimed for use in the method of the invention. Note: The present sequence is not shown in the specification, but was obtained from GenBank using the accession number listed in Table 1 (page 25-33).

Sequence 3224 BP: 820 A; 812 C; 769 G; 823 T; 0 U; 0 Other; XX SO

Query Match	44.3%	Score 542.4;	DB 7;	Length 3224;
Best Local Similarity	69.1%;	Pred. No. 3.9e-147;		
Matches 773:	Conservative	0: Mismatches 336:	Indels	9: Gaps 2

1 ATGGGAGCCACACTTCAAGAAACACACAGTGTTTGATGAAATGCAAGATGTCAACTTTT 60  
65 ATGGCGGGGACCACTCCCAAGACCCCGCGTGTTTGACGAGAAATGAGGAAGTCAACTTT 124  
61 GACCACCTTCAAAATTTTCGAGAGCCATTGGGAAAGGCAGTTTTGGGAAGTCTGCAATGTA 120  
125 GACCAATTTTCAATCTCGCGGCGCAATTGTTAAAGGCGATTTTGGAAAGATGTCATCGTG 184



Copied from 10260845 on 08/11/2005



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 28, 2004, 03:26:42 ; Search time 4804 Seconds  
(without alignments)  
11043.271 Million cell updates/sec

Title: US-10-620-845-8

Perfect score: 1224

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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Sequences: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Date base :

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2: gb.htg.\*

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6: gb.pat.\*

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9: gb.pr.\*

10: gb.ro.\*

11: gb.sts.\*

12: gb.sy.\*

13: gb.un.\*

14: gb.vi.\*

15: em.ba.\*

16: em.fun.\*

17: em.hum.\*

18: em.in.\*

19: em.mu.\*

20: em.om.\*

21: em.or.\*

22: em.ov.\*

23: em.pat.\*

24: em.ph.\*

25: em.pl.\*

26: em.ro.\*

27: em.sts.\*

28: em.un.\*

29: em.vi.\*

30: em.htg.hum.\*

31: em.htg.inv.\*

32: em.htg.other.\*

33: em.htg.mus.\*

34: em.htg.pln.\*

35: em.htg.rod.\*

36: em.htg.mam.\*

37: em.htg.vrt.\*

38: em.sv.\*

39: em.htgo.hum.\*

40: em.htgo.mus.\*

41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1224	100.0	1224	6	AR393902	AR393902 Sequence
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3	1224	100.0	1675	6	AR393904	AR393904 Sequence
4	1224	100.0	1675	6	AX303187	AX303187 Sequence
5	1165.4	95.2	1191	6	AR393903	AR393903 Sequence
6	1165.4	95.2	1191	6	AX303185	AX303185 Sequence
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8	1165.4	95.2	1594	6	AX766348	AX766348 Sequence
9	1163.8	95.1	1191	6	AX320936	AX320936 Sequence
10	1163.8	95.1	1281	6	AX320934	AX320934 Sequence
11	1160.6	94.8	1485	6	AR265353	AR265353 Sequence
12	1160.6	94.8	1485	6	AR432044	AR432044 Sequence
13	1032.2	84.3	2063	6	AX833107	AX833107 Sequence
14	1032.2	84.3	2063	6	AX094580	AX094580 Homo sapi
15	832.8	68.0	981	6	AX166513	AX166513 Sequence
16	773	63.2	4973	10	BC055002	BC055002 Mus muscu
17	661	54.0	711	6	AR393901	AR393901 Sequence
18	661	54.0	711	6	AX303181	AX303181 Sequence
19	660	53.9	678	6	AR393900	AR393900 Sequence
20	660	53.9	678	6	AX303179	AX303179 Sequence
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28	519.6	42.5	3244	6	AX376504	AX376504 Sequence
29	519.6	42.5	3244	9	AY358353	AY358353 Homo sapi
30	497.6	40.7	2184	10	BC026457	BC026457 Mus muscu
31	497.6	40.7	2201	10	AB041542	AB041542 Mus muscu
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39	471.6	38.5	2028	9	BC045760	BC045760 Homo sapi
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41	465.2	38.0	1591	6	AX768900	AX768900 Sequence
42	461.4	37.7	1640	6	AX179651	AX179651 Sequence
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ALIGNMENTS

RESULT 1  
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DEFINITION Sequence 8 from patent US 6617147.  
ACCESSION AR393902  
VERSION AR393902.1 GI:40121077  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1. (bases 1 to 1224)  
AUTHORS Hu, Y., Nepomnichy, B., Wang, X. and Donoho, G.  
TITLE Human kinase proteins and polynucleotides encoding the same  
JOURNAL Patent: US 6617147-A 8 09-SEP-2003;  
FEATURES Location/Qualifiers

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source          1. .1224
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match      100.0%; Score 1224; DB 6; Length 1224;
Best Local Similarity 100.0%; Pred. No. 4.8e-311;
Matches 1224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGGGAGCCCAACCTTCAAGAAACACCACTGTTTTCATGAAATGAAGATGCAACTTT 60
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DB 61 GACCACTTTGAAATTTTGGCGACCATTTGGGAAAGCGCTTTTGGGAAAGTCTGCAATGTA 120
QY 121 CAGGAGATGATACCAAGAGATGTAGCAATGAAGTACATGATTAACAACAAGTGGTG 180
DB 121 CAGGAGATGATACCAAGAGATGTAGCAATGAAGTACATGATTAACAACAAGTGGTG 180
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DB 181 GAGGCAATGAAGTGAAGATGCTTCAAGAACTCCAGATCATGCAAGGTCTGGAGCAC 240
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DB 241 CCTTTCCTGGTTAATTTTGGTATTTCTTCCAGATCAGGAAGACATGTTTCATGGTGGT 300
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421 CGCATCATTCACAGGATATGAAGCTTCACTGTGAGTGTCTCATGCTCCCTGGACTACCTGCGAACGAG 480
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421 CGCATCATTCACAGGGATATGAAGCCTCGACATATTTTACTTTCAGCAACATGGGCACGTG 480

421 CGCATCATTCACAGGGATATGAAGCCTCGACATATTTTACTTTCAGCAACATGGGCACGTG 480

481 CACATCACAGATTTTCAACATTTGCTCGATGCTGCCAGGGAGACACAGATTACCAACATG 540

481 CACATCACAGATTTTCAACATTTGCTCGATGCTGCCAGGGAGACACAGATTACCAACATG 540

541 GCTGSCACCAAGCCTTACATGSCACCTCAGATGTTTCAGCTCCAGAAAGGACGAGCTAT 600

541 GCTGSCACCAAGCCTTACATGSCACCTCAGATGTTTCAGCTCCAGAAAGGACGAGCTAT 600

601 TCCTTTGTCTTGACTGTGTGTCCTGGAGTGACGGCATATGAATCTGTCAGAGGCGCG 660

601 TCCTTTGTCTTGACTGTGTGTCCTGGAGTGACGGCATATGAATCTGTCAGAGGCGCG 660

661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGTACACAGTTTTCAGAG 720

661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGTACACAGTTTTCAGAG 720

721 ACTGTTGTAACTTACCTTCTCCCTGCTCACAGGAAATGGTCTCACTTCTTAAAAAGCTA 780

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901 AATAAAGCGAGGCTGAATTTGTATCCTACTTTTGAACCTTGAGAAATGATTTTGGAGTCC 960

901 AATAAAGCGAGGCTGAATTTGTATCCTACTTTTGAACCTTGAGAAATGATTTTGGAGTCC 960

961 AAACCTTACATAGAAAAAAGCGTCTGGCAAGAGGAGGAGGATATGAGGAATGC 1020

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1021 GATTTCTTCTCAGACATGCTTCTTCAAGAGCACCTTGACTCTGTCCAGAAAGGAGTTTCATA 1080

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1201 TTTTCAGACCTCGAAAGTTTTCATAA 1224

1201 TTTTCAGACCTCGAAAGTTTTCATAA 1224

Copied from 10260845 on 08/11/2005

RESULT 3					
AR393904	Sequence	12 from patent	US 6617147.	1675 bp	DNA
LOCUS	DEFINITION	AR393904			linear
ACCESION	VERSION	AR393904.1	GI:40121081		
KEYWORDS	SOURCE	.			
ORGANISM		Unknown.			
		Unknown.			
		Unclassified.			
REFERENCE		1 (bases 1 to 1675)			
AUTHORS		Hu, Y., Nepomnichy, B., Wang, X. and Doncho, G.			

1313 AATAAAGGAGGCTGAATTTGTGATCTTACCTTTGAACTTTGAGAAATGATTTTGGAGTCC 1372  
961 AARCTTCTACATAAGAAATAAAGAGAGCTCTGGCAAGAGAGAGAGATATGAGAAATGC 1020  
1373 AARCTTCTACATAAGAAATAAAGAGAGCTCTGGCAAGAGAGAGATATGAGAAATGC 1432  
1021 GATTTCTTCCAGACATGTCTTTTCAAGAGCACCTTTGACTCTCTCCAGAGAGTTCATA 1080  
1433 GATTTCTTCCAGACATGTCTTTTCAAGAGCACCTTTGACTCTCTCCAGAGAGTTCATA 1492  
1081 ATTTTCAACAGAGAAAGATTAACAGGACTTTTAAACAAAGACAACCAATCTAGCCTTG 1140  
1493 ATTTTCAACAGAGAAAGATTAACAGGACTTTTAAACAAAGACAACCAATCTAGCCTTG 1552  
1141 GACAAACCAAGAGCCACAGAGTGACAAATGGACAAATGGACACAGACTTCAGTGAGACT 1200  
1553 GACAAACCAAGAGCCACAGAGTGACAAATGGACAAATGGACACAGACTTCAGTGAGACT 1612  
1201 TTTTCAGACCTCGAAAGTTTTCATAA 1224  
1613 TTTTCAGACCTCGAAAGTTTTCATAA 1636  
  
AX303187 1675 bp DNA linear PAT 30-NOV-2001  
Sequence 12 from Patent WO0181557.  
AX303187  
AX303187.1 GI:17383669  
  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Hu, Y., Nepomnichy, B., Wang, X., Donoho, G., Scoville, J. and  
Walke, D.W.  
Human kinase proteins and polynucleotides encoding the same  
Patent: WO 0181557-A 12 01-NOV-2001;  
Lexicon Genetics Incorporated (US)  
Location/Qualifiers  
1. .1675  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
  
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Best Local Similarity 100.0%; Pred. No. 4.9e-311;  
Matches 1224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
1 ATGGAGCCAACTTCAAGAAACACACCAGTGTTCATGAATAATGAGATGCAACTTT 60  
413 ATGGAGCCAACTTCAAGAAACACACCAGTGTTCATGAATAATGAGATGCAACTTT 472  
  
61 GACCACCTTGAAATTTTCGAGCCATTTGGAAAGGCGAGTTTGGGAAGTCTGCATTGTA 120  
473 GACCACCTTGAAATTTTCGAGCCATTTGGGAAGGCGAGTTTGGGAAGTCTGCATTGTA 532  
  
121 CAGAAGAATGATACCAAGAAGATGACGCAATGAAGTACATGAATAAAACAAAGTGGGTG 180  
533 CAGAAGAATGATACCAAGAAGATGACGCAATGAAGTACATGAATAAAACAAAGTGGGTG 592  
  
181 GAGGCGAATGAGTGAGAAATGTCTTCAAGGAACCTCAGATCATGCAGGCTCTGGAGCAC 240  
593 GAGGCGAATGAGTGAGAAATGTCTTCAAGGAACCTCAGATCATGCAGGCTCTGGAGCAC 652  
  
241 CCTTTCCTGGTTAATTTGTGGTATTCTTCCAGATGAGGAACATGTTTCATGGTGGTG 300  
653 CCTTTCCTGGTTAATTTGTGGTATTCTTCCAGATGAGGAACATGTTTCATGGTGGTG 712  
  
301 GACCTCTGCTGGGTGGAGACCTCGCTTATCACCTGCAACAGACGTCACCTTCAAGGAA 360

Unclassified.		1 (bases 1 to 1191)		95.2%; Score 1165.4; DB 6; Length 1191;		0; Mismatches 11; Indels 0; Gaps 0;	
REFERENCE		Hu, Y., Nepomnichy, B., Wang, X. and Donoho, G.		Human kinase proteins and polynucleotides encoding the same		Patent: US 6617147-A 10 09-SEP-2003;	
AUTHORS		Location/Qualifiers		1. .1191		/organism="unknown"	
TITLE		US 6617147-A 10 09-SEP-2003;		/mol_type="genomic DNA"			
JOURNAL							
FEATURES		source					
ORIGIN							
Query Match		95.2%; Score 1165.4; DB 6; Length 1191;		Best Local Similarity		99.1%; Pred. No. 1.3e-295;	
Matches 1172; Conservative		0; Mismatches 11; Indels 0; Gaps 0;					
Qy	1	ATGGGAGCCCAACACCTTCAAGAAACCCACGCTGTTGATGAAATGAAGATGTCAACTTT	60	1	ATGGGAGCCCAACACCTTCAAGAAACCCACGCTGTTGATGAAATGAAGATGTCAACTTT	60	
Db	1	ATGGGAGCCCAACACCTTCAAGAAACCCACGCTGTTGATGAAATGAAGATGTCAACTTT	60	1	ATGGGAGCCCAACACCTTCAAGAAACCCACGCTGTTGATGAAATGAAGATGTCAACTTT	60	
Qy	61	GACCACTTTGAAATTTTCGAGCATTGGGAAAGCGAGTTTGGGAAAGTCTGCATTGTA	120	61	GACCACTTTGAAATTTTCGAGCATTGGGAAAGCGAGTTTGGGAAAGTCTGCATTGTA	120	
Db	61	GACCACTTTGAAATTTTCGAGCATTGGGAAAGCGAGTTTGGGAAAGTCTGCATTGTA	120	61	GACCACTTTGAAATTTTCGAGCATTGGGAAAGCGAGTTTGGGAAAGTCTGCATTGTA	120	
Qy	121	CAGAGATGATACCAAGAAAGTACGCAATGAGTACATGATGAATGAATGAAGTGGTG	180	121	CAGAGATGATACCAAGAAAGTACGCAATGAGTACATGATGAATGAATGAAGTGGTG	180	
Db	121	CAGAGATGATACCAAGAAAGTACGCAATGAGTACATGATGAATGAATGAAGTGGTG	180	121	CAGAGATGATACCAAGAAAGTACGCAATGAGTACATGATGAATGAATGAAGTGGTG	180	
Qy	181	GAGCGCAATGAGTGAAGTGAAGTGTCTTCAAGAAATGCTCCAGATCATCGAGGCTCTGAGCAC	240	181	GAGCGCAATGAGTGAAGTGAAGTGTCTTCAAGAAATGCTCCAGATCATCGAGGCTCTGAGCAC	240	
Db	181	GAGCGCAATGAGTGAAGTGAAGTGTCTTCAAGAAATGCTCCAGATCATCGAGGCTCTGAGCAC	240	181	GAGCGCAATGAGTGAAGTGAAGTGTCTTCAAGAAATGCTCCAGATCATCGAGGCTCTGAGCAC	240	
Qy	241	CTCGAACCTAATCCAGACCAAGTATTTCTCAGTTATCTGATGATCCAGAACTCCCGTAT	840	241	CTCGAACCTAATCCAGACCAAGTATTTCTCAGTTATCTGATGATCCAGAACTCCCGTAT	840	
Db	241	CTCGAACCTAATCCAGACCAAGTATTTCTCAGTTATCTGATGATCCAGAACTCCCGTAT	840	241	CTCGAACCTAATCCAGACCAAGTATTTCTCAGTTATCTGATGATCCAGAACTCCCGTAT	840	
Qy	841	ATGAATGATATAAATCGGATGCGATTTTTCAGAGAGGCTCATTCAGAGTTTCATTCCT	900	841	ATGAATGATATAAATCGGATGCGATTTTTCAGAGAGGCTCATTCAGAGTTTCATTCCT	900	
Db	841	ATGAATGATATAAATCGGATGCGATTTTTCAGAGAGGCTCATTCAGAGTTTCATTCCT	900	841	ATGAATGATATAAATCGGATGCGATTTTTCAGAGAGGCTCATTCAGAGTTTCATTCCT	900	
RESULT 6		AX303185		1191 bp		DNA	
LOCUS		Sequence 10 from Patent WO0181557.		linear		PAT 30-NOV-2001	
DEFINITION		AX303185					
ACCESSION		AX303185					
VERSION		AX303185.1		GI:17383668			
KEYWORDS		Homo sapiens (human)					
SOURCE		Homo sapiens					
ORGANISM		Homo sapiens					
REFERENCE		Hu, Y., Nepomnichy, B., Wang, X., Donoho, G., Scoville, J. and		Walke, D.W.			
AUTHORS		Human kinase proteins and polynucleotides encoding the same		Patent: WO 0181557-A 10 01-NOV-2001;			
TITLE		Lexicon Genetics Incorporated (US)					
JOURNAL		Location/Qualifiers		1. .1191		/organism="Homo sapiens"	
FEATURES		source				/mol_type="unassigned DNA"	
ORIGIN						/db_xref="taxon:9606"	
Query Match		95.2%; Score 1165.4; DB 6; Length 1191;		Best Local Similarity		99.1%; Pred. No. 1.3e-295;	
Matches 1172; Conservative		0; Mismatches 11; Indels 0; Gaps 0;					
Qy	1	ATGGGAGCCCAACACCTTCAAGAAACCCACGCTGTTGATGAAATGAAGATGTCAACTTT	60	1	ATGGGAGCCCAACACCTTCAAGAAACCCACGCTGTTGATGAAATGAAGATGTCAACTTT	60	
Db	1	ATGGGAGCCCAACACCTTCAAGAAACCCACGCTGTTGATGAAATGAAGATGTCAACTTT	60	1	ATGGGAGCCCAACACCTTCAAGAAACCCACGCTGTTGATGAAATGAAGATGTCAACTTT	60	
Qy	61	GACCACTTTGAAATTTTCGAGCATTGGGAAAGCGAGTTTGGGAAAGTCTGCATTGTA	120	61	GACCACTTTGAAATTTTCGAGCATTGGGAAAGCGAGTTTGGGAAAGTCTGCATTGTA	120	
Db	61	GACCACTTTGAAATTTTCGAGCATTGGGAAAGCGAGTTTGGGAAAGTCTGCATTGTA	120	61	GACCACTTTGAAATTTTCGAGCATTGGGAAAGCGAGTTTGGGAAAGTCTGCATTGTA	120	
Qy	121	CAGAGATGATACCAAGAAAGTACGCAATGAGTACATGATGAATGAATGAAGTGGTG	180	121	CAGAGATGATACCAAGAAAGTACGCAATGAGTACATGATGAATGAATGAAGTGGTG	180	
Db	121	CAGAGATGATACCAAGAAAGTACGCAATGAGTACATGATGAATGAATGAAGTGGTG	180	121	CAGAGATGATACCAAGAAAGTACGCAATGAGTACATGATGAATGAATGAAGTGGTG	180	
Qy	181	GAGCGCAATGAGTGAAGTGAAGTGTCTTCAAGAAATGCTCCAGATCATCGAGGCTCTGAGCAC	240	181	GAGCGCAATGAGTGAAGTGAAGTGTCTTCAAGAAATGCTCCAGATCATCGAGGCTCTGAGCAC	240	
Db	181	GAGCGCAATGAGTGAAGTGAAGTGTCTTCAAGAAATGCTCCAGATCATCGAGGCTCTGAGCAC	240	181	GAGCGCAATGAGTGAAGTGAAGTGTCTTCAAGAAATGCTCCAGATCATCGAGGCTCTGAGCAC	240	
Qy	241	CTCGAACCTAATCCAGACCAAGTATTTCTCAGTTATCTGATGATCCAGAACTCCCGTAT	840	241	CTCGAACCTAATCCAGACCAAGTATTTCTCAGTTATCTGATGATCCAGAACTCCCGTAT	840	
Db	241	CTCGAACCTAATCCAGACCAAGTATTTCTCAGTTATCTGATGATCCAGAACTCCCGTAT	840	241	CTCGAACCTAATCCAGACCAAGTATTTCTCAGTTATCTGATGATCCAGAACTCCCGTAT	840	
Qy	841	ATGAATGATATAAATCGGATGCGATTTTTCAGAGAGGCTCATTCAGAGTTTCATTCCT	900	841	ATGAATGATATAAATCGGATGCGATTTTTCAGAGAGGCTCATTCAGAGTTTCATTCCT	900	
Db	841	ATGAATGATATAAATCGGATGCGATTTTTCAGAGAGGCTCATTCAGAGTTTCATTCCT	900	841	ATGAATGATATAAATCGGATGCGATTTTTCAGAGAGGCTCATTCAGAGTTTCATTCCT	900	







```

REFERENCE
AUTHORS      Meyers, R. and Hunter, J.J.
TITLE        14911 novel protein kinase molecules and uses therefor
JOURNAL      Patent: WO 0181589-A 3 01-NOV-2001;
              Millennium Pharmaceuticals, Inc. (US)
FEATURES
source       Location/Qualifiers
              1. .1191
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

ORIGIN
Query Match      95.1%; Score 1163.8; DB 6; Length 1191;
Best Local Similarity 99.0%; Pred. No. 3.4e-295;
Matches 1171; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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61  GACCACCTTGAATTTTGGAGCCATTTGGGAAAGCGCAGTTTTTGGGAAAGTCTGCATTGTA 120
   |||||
61  GACCACCTTGAATTTTGGAGCCATTTGGGAAAGCGCAGTTTTTGGGAAAGTCTGCATTGTA 120
   |||||
121  CAGAAGATGATCAAGAAAGATGTAGCGATGAAGTACATGAATTAACAAAGTGGGTG 180
   |||||
121  CAGAAGATGATCAAGAAAGATGTAGCGATGAAGTACATGAATTAACAAAGTGGGTG 180
   |||||
181  GAGCGCAATGAAGTGAAGATGCTTCAAGAAACCTCAGATCATGACAGGCTCTGGAGCAC 240
   |||||
181  GAGCGCAATGAAGTGAAGATGCTTCAAGAAACCTCAGATCATGACAGGCTCTGGAGCAC 240
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   |||||
241  CTTTCTCTGTTAATTTGGTGTATCTCTCAAGATGAGGAAGACATGTTTCATGGTGGTG 300
   |||||
301  GACTCTCTGCTGGTGAGACCTCGGTATACCTGCAACAGAACGTCACATTCAGAGAA 360
   |||||
301  GACTCTCTGCTGGTGAGACCTCGGTATACCTGCAACAGAACGTCACATTCAGAGAA 360
   |||||
361  GAAACAGTGAAGCTCTTCATCTGTGAGCTGGTATGCTGATGCTGCTGATGCTGCAAGCAC 420
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361  GAAACAGTGAAGCTCTTCATCTGTGAGCTGGTATGCTGATGCTGCTGATGCTGCAAGCAC 420
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421  CGCATCATTCACAGGGATGAAGCCTGACAAATATTTTACTTGAAGAACATGGSCACGTG 480
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481  CACATCAAGATTTCAACATGCTGGATGCTGCCAGGAGACACACAGATACCAACATG 540
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541  GCTGGACCAAGCCTTACATGGACCTGAGATGTTCAAGTCCAGAAAGAGCAGGCTAT 600
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781  CTCGAACTAATCCAGACCAACGATTTTCTCAGTATTCATGATGTCAGAACTTCCCGTAT 840
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RESULT 10
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DEFINITION    Sequence 1 from Patent WO0181589.
ACCESSION     AX320934
VERSION        AX320934.1 GI:17902480
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Meyers, R. and Hunter, J.J.
TITLES         14911 novel protein kinase molecules and uses therefor
JOURNAL        Patent: WO 0181589-A 1 01-NOV-2001;
               Millennium Pharmaceuticals, Inc. (US)
FEATURES
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               HTFDNIAAMLPREIOITWAGTKPYKAMPESRRKAGYSPAVDMWSLGVTAVELLR
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Query Match      95.1%; Score 1163.8; DB 6; Length 1281;
Best Local Similarity 99.0%; Pred. No. 3.4e-295;
Matches 1171; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

1  ATGGAGCCACACCTTCAAGAAACACACACAGTGTTCATGAATGAAGATGTCACATTT 60
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61  GACCACCTTGAATTTTGGAGCCATTTGGGAAAGCGCAGTTTTTGGGAAAGTCTGCATTGTA 120
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RESULT 11	AR265353	LOCUS	Sequence 1	1485 bp	DNA	linear	PAT 10-APR-2003	
DEFINITION	AR265353	1	from patent US 6492155.					
ACCESSION	AR265353							
VERSION	AR265353.1	GI:29693863						
KEYWORDS	Unknown.							
SOURCE	Unknown.							
ORGANISM	Unclassified.							
REFERENCE	1. (bases 1 to 1485)							
AUTHORS	Ye, J., Yan, C., Di Francesco, V. and Beasley, E. M.							
TITLE	Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof							
JOURNAL	Patent: US 6492155-A 1 10-DEC-2002;							
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Best Local Similarity	98.8%;	Pred. No.	2.4e-294;					
Matches 1169;	Conservative	0;	Mismatches	14;	Indels	0;	Gaps	0;
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QY	12.. CAGAAGAATGATACCAAGAAGATGTACG	CAATGAAGTACATGAATAAAACAAAAGTCGCTG	180					
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QY	181.. GAGCGCAATGAAGTGAGAAATGCTTTCA	AGAACTCCAGATCATGCAGGGTCTGGAGCAC	240					
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QY	241.. CTTTTCCTGTTAAATTTGTGGTATTCTT	CCAAGATGAGGAAGACATGTTCAATGTTGGTG	300					
Db	243.. CTTTTCCTGTTAAATTTGTGGTATTCTT	CCAAGATGAGGAAGACATGTTCAATGTTGGTG	302					
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Db	303.. GACCTCTCTGGGTGGAGACCTGGTGTAT	CACTTCAAGAACAGACGTCACCTTCAAGGAA	362					
QY	361.. GAAACAGTGAGCTCTTCATCTGTGAGCT	GTGTATGCGCCCTGGACTACTCTGAGAACAG	420					
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Db	423.. CGCATCTTACAGGGATATGAAGCCTGCA	CAATATTTTACTTGACGAACATGGGCACTG	482					
QY	481.. CACATCAAGATTTCAACATTTCTCGATG	TGTCGCCAGGAGACACAGATTACCACTG	540					
Db	483.. CACATCAAGATTTCAACATTTCTCGATG	TGTCGCCAGGAGACACAGATTACCACTG	542					
QY	541.. GCTGGCACCAAGCCTTACATGGCACTTGA	GTGTTTACGCTCCAGAAAGGACGAGCTAT	600					
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QY	601.. TCCTTTGCTGTTGACTGTGTGTCCTGGAG	TGACGGCATATGAAGTCTCTGAGAGCCGG	660					
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QY	661.. AGACCGTATCATATTCGCTCCAGTACTTCC	AGAAAGAAATTTGTAACACAGTTTGAGACG	720					
Db	663.. AGACCGTATCATATTCGCTCCAGTACTTCC	AGAAAGAAATTTGTAACACAGTTTGAGACG	722					

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 843 ATGAATGATATAAATCTGGGATGAGTTTCTCAGAGAGGCTCATTCAGAGTTTCATTCCT 902  
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 LOCUS Sequence 1 from patent US 6653117.  
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 ACCESSION AR432044  
 VERSION AR432044.1 GI:40194241  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 UNCLASSIFIED.  
 REFERENCE 1 (bases 1 to 1485)  
 AUTHORS Ye, J., Yan, C., Di Francesco, V. and Beasley, E. M.  
 TITLE Isolated human kinase proteins  
 JOURNAL Patent: US 6653117-A 1 25-NOV-2003;  
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Query Match 94.8%; Score 1160.6; DB 6; Length 1485;  
 Best Local Similarity 98.8%; Pred. No. 2.4e-294;  
 Matches 1169; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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241 CTTTCTCTGTTTAAATTTGTGGTATTTCTTCCAGATGAGGAAGACATGTTTCATGTTGGTG 300  
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 661 AGACGCTATCATATTCGCTCCAGTCTTCCAGAGGAAATTTGTCACACGTTTGGAGCG 720  
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 DEFINITION AX833107  
 ACCESSION AX833107  
 VERSION AX833107.1 GI:39919242  
 KEYWORDS Homo sapiens (human)  
 SOURCE

Copied from 10260845 on 08/11/2005

Query Match	84.3%	Score 1032.2;	DB 9;	Length 2063;
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Matches 1034;	Conservative	Pred. No. 1.6e-260;		
		0;	Mismatches 3;	Indels 0;
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 QY 1054 ACTGTTGTAATTAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1113  
 Db  
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RESULT 15  
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 DEFINITION  
 Sequence 4 from Patent WO0138503.  
 AX166513  
 ACCESSION  
 VERSION  
 AX166513.1 GI:14546858  
 KEYWORDS  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 AUTHORS  
 Plowman, G.D., Whyte, D., Manning, G.S., Sudarsanam, S.S., Martinez, R.,  
 Flanagan, P. and Clary, D.S.  
 TITLE  
 Novel human protein kinases and protein kinase-like enzymes  
 JOURNAL  
 Patent: WO 0138503-A 4 31-MAY-2001;  
 Sugen, Inc. (US)  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 28, 2004, 05:36:39 ; Search time 3064 Seconds

(without alignments)  
11929.278 Million cell updates/sec

Title: US-10-620-845-8

Perfect score: 1224

Sequence: 1 atggagagccacacttcaag.....agactcgaaagtattcataa 1224

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Sequenced: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Datebase :

EST:\*

1: em estba:\*

2: em esthum:\*

3: em estin:\*

4: em estmu:\*

5: em estov:\*

6: em estpl:\*

7: em estro:\*

8: em htc:\*

9: gb est1:\*

10: gb est2:\*

11: gb htc:\*

12: gb est3:\*

13: gb est4:\*

14: gb est5:\*

15: em estfun:\*

16: em estom:\*

17: em gss hum:\*

18: em gss inv:\*

19: em gss pin:\*

20: em gss vrt:\*

21: em gss fun:\*

22: em gss nam:\*

23: em gss mus:\*

24: em gss pro:\*

25: em gss rod:\*

26: em gss phg:\*

27: em gss vrl:\*

28: gb gss1:\*

29: gb gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	948.6	77.5	1927	11 AK042599	AK042599 Mus muscu
2	948.6	77.5	2477	11 AK044474	AK044474 Mus muscu
3	948.6	77.5	3766	11 AK036266	AK036266 Mus muscu
4	710.6	58.1	893	10 BG036777	BG036777 602286992

## ALIGNMENTS

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AK042599  
LOCUS  
DEFINITION

AK042599 1927 bp mRNA linear HTC 19-SEP-2003  
Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length  
enriched library, clone:AV30009C22 product:SIMILAR TO SERINE  
THREONINE KINASE 32 homolog [Homo sapiens], full insert sequence.

ACCESSION AK042599  
VERSION AK042599.1 GI:26335202  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Chordata; Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.

REFERENCE 1  
AUTHORS Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636

REFERENCE 2  
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PUBMED 11042159

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C

REFERENCE  
AUTHORS

3 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,  
Kono,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,  
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,  
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,  
Fujisake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,S., Watahiki,M.,  
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura,S., Kawai,J.,  
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multipicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861

REFERENCE  
AUTHORS

4 The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

JOURNAL  
REFERENCE

5 The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 1927)

JOURNAL  
REFERENCE

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,  
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,  
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,  
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,  
Kato,H., Kawai,J., Kojima,Y., Kondo,S., Komno,H., Kouda,M.,  
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,  
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,  
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,  
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,  
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,P., Takaku-Akahira,S.,  
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,  
Muramatsu,M. and Hayashizaki,Y.  
Direct Submission

JOURNAL  
REFERENCE

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)

## COMMENT

cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/  
URL: http://fantom.gsc.riken.go.jp/.

FEATURES  
source

Location/Qualifiers  
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QQNNNL"

## ORIGIN

Query Match: 77.5%; Score 948.6; DB 11; Length 1927;  
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QY 121 CAGAAAGATGATACCAAGAAGATGTACGCAATGAAGTACATCAATAACCAAAAGTGCCTG 180  
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 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitho, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tomaru, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.  
 Direct Submission  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
 CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Retina RNA was provided by Dr. Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged. Please visit our web site for further details.  
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 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning  
 Meth. Enzymol. 303, 19-44 (1999)  
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 High-efficiency full-length cDNA cloning  
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 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
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 Normalization and subtraction of cap-trapper-selected cDNAs to  
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 Genome Res. 10 (10), 1617-1630 (2000)  
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 RIKEN integrated sequence analysis (RISA) system--384-format  
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 Genome Res. 10 (11), 1757-1771 (2000)  
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 5  
 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409, 685-690 (2001)  
 6  
 The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 7  
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
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 Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,  
 URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
 Fax:81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: <http://genome.gsc.riken.go.jp/>  
URL: <http://fantom.gsc.riken.go.jp/>

# FEATURES

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REFERENCE 1 (bases 1 to 893)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-k@mail.nih.gov](mailto:cgabs-k@mail.nih.gov)  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

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## RESULT 5

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LOCUS Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length  
DEFINITION enriched library, clone:C230053G02 product:serine threonine kinase  
32, full insert sequence.  
ACCESSION AK082468  
VERSION AK082468.1 GI:26349720  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
99279253 PUBLISHED 10349636  
2  
REFERENCE  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Komano, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
20499374 PUBLISHED 11042159  
3  
REFERENCE  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Komano, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
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Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multipillar sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913 PUBLISHED 11076861  
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REFERENCE  
The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)  
5  
REFERENCE  
The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
5 (bases 1 to 3439)  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
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Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,

Muramatsu, M. and Hayashizaki, Y.

Direct Submission  
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.go.jp/  
URL: http://phantom.gsc.riken.go.jp/  
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VERSION AY406286.1 GI:39762260  
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ORGANISM Mus musculus  
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1 (bases 1 to 1245)  
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarwal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,



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Mus musculus  
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JOURNAL







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            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
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            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
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directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."

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/2005



ORGANISM Mus musculus  
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 711)  
REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Dr. Jim Lin, University of Iowa  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGC clone distribution information can be  
found through the i.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)  
Seq primer: pYX-5.  
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1996. Denatured RNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with oligo-dT  
primer containing a Not I site. Double strand cDNA was  
size selected according to mRNA size fraction, ligated  
with EcoR I adaptor, digested with NotI and then cloned  
directionally into pYX-Asc vector. The library tag  
sequence located between the Not I site and the polyA tail  
is AGCGAGACAG. This library was created for the University  
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
Developing Mouse Nervous System', supported by National  
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,  
program coordinator."

FEATURES  
source

Location/Qualifiers

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program coordinator."

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